



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 126843

TO: Patricia Duffy  
Location: rem/3b05/3c18  
Art Unit: 1645  
Monday, July 19, 2004

Case Serial Number: 09/932613

From: Mary Jane Ruhl  
Location: Biotech-Chem Library  
Remsen 1-A-62  
Phone: 571-272-2524

maryjane.ruhl@uspto.gov

### Search Notes

Examiner Duffy,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl  
Technical Information Specialist  
STIC  
Remsen 1-A-62  
Ext. 22524

*send to scanning*



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STIC-Biotech/ChemLib

126843

my

From: Duffy, Patricia  
Sent: Sunday, July 11, 2004 10:30 AM  
To: STIC-Biotech/ChemLib  
Subject: Sequence search 09/932,613

Importance: High

Please search SEQ ID NO:457 in the commercial and interference databases.  
Please print out top 100 hits.

Thanks.

Patricia A. Duffy, Ph.D.  
Art Unit 1645, Remsen 3B05  
571-272-0855

STIC  
JUL 12 2004  
10:30 AM

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 12, 2004, 21:21:26 ; Search time 54 Seconds

(without alignments)  
52.324 Million cell updates/sec

Title: US-09-932-613-457

Perfect score: 64

Sequence: 1 WYDPLTKML 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : A\_Geneseq\_29Jan04:\*

1: geneseqp1980s:\*  
2: geneseqp2000s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	10	5	ABJ00997 B lymphoc
2	64	100.0	10	5	ABJ00977 B lymphoc
3	64	100.0	10	5	ABJ00977 B lymphoc
4	64	100.0	10	5	ABJ00977 B lymphoc
5	64	100.0	10	5	ABJ00977 B lymphoc
6	64	100.0	10	5	ABJ00977 B lymphoc
7	64	100.0	10	5	ABJ00977 B lymphoc
8	64	100.0	10	5	ABJ00977 B lymphoc
9	64	100.0	10	5	ABJ00977 B lymphoc
10	64	100.0	10	5	ABJ00977 B lymphoc
11	64	100.0	10	5	ABJ00977 B lymphoc
12	64	100.0	10	5	ABJ00977 B lymphoc
13	64	100.0	10	5	ABJ00977 B lymphoc
14	64	100.0	10	5	ABJ00977 B lymphoc
15	64	100.0	10	5	ABJ00977 B lymphoc
16	64	100.0	10	5	ABJ00977 B lymphoc
17	64	100.0	10	5	ABJ00977 B lymphoc
18	64	100.0	10	5	ABJ00977 B lymphoc
19	64	100.0	10	5	ABJ00977 B lymphoc
20	64	100.0	10	5	ABJ00977 B lymphoc
21	64	100.0	10	5	ABJ00977 B lymphoc
22	64	100.0	10	5	ABJ00977 B lymphoc
23	64	100.0	10	5	ABJ00977 B lymphoc
24	64	100.0	10	5	ABJ00977 B lymphoc
25	64	100.0	10	5	ABJ00977 B lymphoc

99	64	100.0	14	5	ABJ00778	ABJ00778	B	Lymphoc	172	64	100.0	14	5	ABG33676	ABG33676	B	Lymphoc
100	64	100.0	14	5	ABJ00796	ABJ00796	B	Lymphoc	173	64	100.0	14	5	ABG33591	ABG33591	B	Lymphoc
101	64	100.0	14	5	ABJ00810	ABJ00810	B	Lymphoc	174	64	100.0	14	5	ABG33594	ABG33594	B	Lymphoc
102	64	100.0	14	5	ABJ00837	ABJ00837	B	Lymphoc	175	64	100.0	14	5	ABG33623	ABG33623	B	Lymphoc
103	64	100.0	14	5	ABJ00746	ABJ00746	B	Lymphoc	176	64	100.0	14	5	ABG33629	ABG33629	B	Lymphoc
104	64	100.0	14	5	ABJ00764	ABJ00764	B	Lymphoc	177	64	100.0	14	5	ABG33631	ABG33631	B	Lymphoc
105	64	100.0	14	5	ABJ00783	ABJ00783	B	Lymphoc	178	64	100.0	14	5	ABG33635	ABG33635	B	Lymphoc
106	64	100.0	14	5	ABJ00799	ABJ00799	B	Lymphoc	179	64	100.0	14	5	ABG33688	ABG33688	B	Lymphoc
107	64	100.0	14	5	ABJ00801	ABJ00801	B	Lymphoc	180	64	100.0	14	5	ABG33691	ABG33691	B	Lymphoc
108	64	100.0	14	5	ABJ00823	ABJ00823	B	Lymphoc	181	64	100.0	14	5	ABG33621	ABG33621	B	Lymphoc
109	64	100.0	14	5	ABJ00727	ABJ00727	B	Lymphoc	182	64	100.0	14	5	ABG33628	ABG33628	B	Lymphoc
110	64	100.0	14	5	ABJ00733	ABJ00733	B	Lymphoc	183	64	100.0	14	5	ABG33671	ABG33671	B	Lymphoc
111	64	100.0	14	5	ABJ00748	ABJ00748	B	Lymphoc	184	64	100.0	14	5	ABG33674	ABG33674	B	Lymphoc
112	64	100.0	14	5	ABJ00753	ABJ00753	B	Lymphoc	185	64	100.0	14	5	ABG33589	ABG33589	B	Lymphoc
113	64	100.0	14	5	ABJ00765	ABJ00765	B	Lymphoc	186	64	100.0	14	5	ABG33600	ABG33600	B	Lymphoc
114	64	100.0	14	5	ABJ00768	ABJ00768	B	Lymphoc	187	64	100.0	14	5	ABG33611	ABG33611	B	Lymphoc
115	64	100.0	14	5	ABJ00797	ABJ00797	B	Lymphoc	188	64	100.0	14	5	ABG33654	ABG33654	B	Lymphoc
116	64	100.0	14	5	ABJ00800	ABJ00800	B	Lymphoc	189	64	100.0	14	5	ABG33659	ABG33659	B	Lymphoc
117	64	100.0	14	5	ABJ00805	ABJ00805	B	Lymphoc	190	64	100.0	14	5	ABG33654	ABG33654	B	Lymphoc
118	64	100.0	14	5	ABJ00808	ABJ00808	B	Lymphoc	191	64	100.0	14	5	ABG33655	ABG33655	B	Lymphoc
119	64	100.0	14	5	ABJ00813	ABJ00813	B	Lymphoc	192	64	100.0	14	5	ABG33596	ABG33596	B	Lymphoc
120	64	100.0	14	5	ABJ00814	ABJ00814	B	Lymphoc	193	64	100.0	14	5	ABG33624	ABG33624	B	Lymphoc
121	64	100.0	14	5	ABG33595	ABG33595	B	Lymphoc	194	64	100.0	14	5	ABG33615	ABG33615	B	Lymphoc
122	64	100.0	14	5	ABG33606	ABG33606	B	Lymphoc	195	64	100.0	14	5	ABG33652	ABG33652	B	Lymphoc
123	64	100.0	14	5	ABG33616	ABG33616	B	Lymphoc	196	64	100.0	14	5	ABG33666	ABG33666	B	Lymphoc
124	64	100.0	14	5	ABG33634	ABG33634	B	Lymphoc	197	64	100.0	14	5	ABG33678	ABG33678	B	Lymphoc
125	64	100.0	14	5	ABG33656	ABG33656	B	Lymphoc	198	64	100.0	14	5	ABG33684	ABG33684	B	Lymphoc
126	64	100.0	14	5	ABG33667	ABG33667	B	Lymphoc	199	64	100.0	14	5	ABG33689	ABG33689	B	Lymphoc
127	64	100.0	14	5	ABG33687	ABG33687	B	Lymphoc	200	64	100.0	14	5	ABG33696	ABG33696	B	Lymphoc
128	64	100.0	14	5	ABG33598	ABG33598	B	Lymphoc	201	64	100.0	14	5	ABG33588	ABG33588	B	Lymphoc
129	64	100.0	14	5	ABG33632	ABG33632	B	Lymphoc	202	64	100.0	14	5	ABG33603	ABG33603	B	Lymphoc
130	64	100.0	14	5	ABG33644	ABG33644	B	Lymphoc	203	64	100.0	14	5	ABG33618	ABG33618	B	Lymphoc
131	64	100.0	14	5	ABG33679	ABG33679	B	Lymphoc	204	64	100.0	14	5	ABG33609	ABG33609	B	Lymphoc
132	64	100.0	14	5	ABG33697	ABG33697	B	Lymphoc	205	64	100.0	14	5	ABG33648	ABG33648	B	Lymphoc
133	64	100.0	14	5	ABG33677	ABG33677	B	Lymphoc	206	64	100.0	14	5	ABG33669	ABG33669	B	Lymphoc
134	64	100.0	14	5	ABG33632	ABG33632	B	Lymphoc	207	64	100.0	14	5	ABG33592	ABG33592	B	Lymphoc
135	64	100.0	14	5	ABG33639	ABG33639	B	Lymphoc	208	64	100.0	14	5	ABG33614	ABG33614	B	Lymphoc
136	64	100.0	14	5	ABG33665	ABG33665	B	Lymphoc	209	64	100.0	14	5	ABG33620	ABG33620	B	Lymphoc
137	64	100.0	14	5	ABG33677	ABG33677	B	Lymphoc	210	64	100.0	14	5	ABG33637	ABG33637	B	Lymphoc
138	64	100.0	14	5	ABG33661	ABG33661	B	Lymphoc	211	64	100.0	14	5	ABG33664	ABG33664	B	Lymphoc
139	64	100.0	14	5	ABG33681	ABG33681	B	Lymphoc	212	64	100.0	14	5	ABG33675	ABG33675	B	Lymphoc
140	64	100.0	14	5	ABG33698	ABG33698	B	Lymphoc	213	64	100.0	14	5	ABG33687	ABG33687	B	Lymphoc
141	64	100.0	14	5	ABG33619	ABG33619	B	Lymphoc	214	64	100.0	14	5	ABG33693	ABG33693	B	Lymphoc
142	64	100.0	14	5	ABG33602	ABG33602	B	Lymphoc	215	64	100.0	14	5	ABG33599	ABG33599	B	Lymphoc
143	64	100.0	14	5	ABG33636	ABG33636	B	Lymphoc	216	64	100.0	14	5	ABG33601	ABG33601	B	Lymphoc
144	64	100.0	14	5	ABG33619	ABG33619	B	Lymphoc	217	64	100.0	14	5	ABG33612	ABG33612	B	Lymphoc
145	64	100.0	14	5	ABG33636	ABG33636	B	Lymphoc	218	64	100.0	14	5	ABG33613	ABG33613	B	Lymphoc
146	64	100.0	14	5	ABG33641	ABG33641	B	Lymphoc	219	64	100.0	14	5	ABG33625	ABG33625	B	Lymphoc
147	64	100.0	14	5	ABG33661	ABG33661	B	Lymphoc	220	64	100.0	14	5	ABG33680	ABG33680	B	Lymphoc
148	64	100.0	14	5	ABG33670	ABG33670	B	Lymphoc	221	64	100.0	14	5	ABG33686	ABG33686	B	Lymphoc
149	64	100.0	14	5	ABG33683	ABG33683	B	Lymphoc	222	64	100.0	14	5	ABG33690	ABG33690	B	Lymphoc
150	64	100.0	14	5	ABG33607	ABG33607	B	Lymphoc	223	64	100.0	14	5	ABG33697	ABG33697	B	Lymphoc
151	64	100.0	14	5	ABG33672	ABG33672	B	Lymphoc	224	64	100.0	14	5	ABG33708	ABG33708	B	Lymphoc
152	64	100.0	14	5	ABG33673	ABG33673	B	Lymphoc	225	64	100.0	14	5	ABG33842	ABG33842	B	Lymphoc
153	64	100.0	14	5	ABG33682	ABG33682	B	Lymphoc	226	64	100.0	14	5	ABG33848	ABG33848	B	Lymphoc
154	64	100.0	14	5	ABG33692	ABG33692	B	Lymphoc	227	64	100.0	14	5	ABG33889	ABG33889	B	Lymphoc
155	64	100.0	14	5	ABG33699	ABG33699	B	Lymphoc	228	64	100.0	14	5	ABG33926	ABG33926	B	Lymphoc
156	64	100.0	14	5	ABG33658	ABG33658	B	Lymphoc	229	64	100.0	14	5	ABG33931	ABG33931	B	Lymphoc
157	64	100.0	14	5	ABG33662	ABG33662	B	Lymphoc	230	64	100.0	14	5	ABG33930	ABG33930	B	Lymphoc
158	64	100.0	14	5	ABG33657	ABG33657	B	Lymphoc	231	64	100.0	14	5	ABG33927	ABG33927	B	Lymphoc
159	64	100.0	14	5	ABG33608	ABG33608	B	Lymphoc	232	64	100.0	14	5	ABG33928	ABG33928	B	Lymphoc
160	64	100.0	14	5	ABG33617	ABG33617	B	Lymphoc	233	64	100.0	14	5	ABG33929	ABG33929	B	Lymphoc
161	64	100.0	14	5	ABG33626	ABG33626	B	Lymphoc	234	64	100.0	14	5	ABG33930	ABG33930	B	Lymphoc
162	64	100.0	14	5	ABG33633	ABG33633	B	Lymphoc	235	64	100.0	14	5	ABG33931	ABG33931	B	Lymphoc
163	64	100.0	14	5	ABG33650	ABG33650	B	Lymphoc	236	64	100.0	14	5	ABG33932	ABG33932	B	Lymphoc
164	64	100.0	14	5	ABG33651	ABG33651	B	Lymphoc	237	64	100.0	14	5	ABG33933	ABG33933	B	Lymphoc
165	64	100.0	14	5	ABG33657	ABG33657	B	Lymphoc	238	64	100.0	14	5	ABG33934	ABG33934	B	Lymphoc
166	64	100.0	14	5	ABG33658	ABG33658	B	Lymphoc	239	64	100.0	14	5	ABG33935	ABG33935	B	Lymphoc
167	64	100.0	14	5	ABG33662	ABG33662	B	Lymphoc	240	64	100.0	14	5	ABG33936	ABG33936	B	Lymphoc
168	64	100.0	14	5	ABG33693	ABG33693	B	Lymphoc	241	64	100.0	14	5	ABG33937	ABG33937	B	Lymphoc
169	64	100.0	14	5	ABG33695	ABG33695	B	Lymphoc	242	64	100.0	14	5	ABG33938	ABG33938	B	Lymphoc
170	64	100.0	14	5	ABG33645	ABG33645	B	Lymphoc	243	64	100.0	14	5	ABG33939	ABG33939	B	Lymphoc
171	64	100.0	14	5	ABG33653	ABG33653	B	Lymphoc	244	64	100.0	14	5	ABG33940	ABG33940	B	Lymphoc

245	62	96.9	14	5	ABG33787	Abg33787 B Lymphoc
246	62	96.9	14	5	ABG33789	Abg33789 B Lymphoc
247	62	96.9	14	5	ABG33790	Abg33790 B Lymphoc
248	62	96.9	14	5	ABG33792	Abg33792 B Lymphoc
249	62	96.9	14	5	ABG33788	Abg33788 B Lymphoc
250	62	96.9	14	5	ABG33791	Abg33791 B Lymphoc
251	61	95.3	14	5	ABJ00916	Abj00916 B Lymphoc
252	61	95.3	14	5	ABJ00918	Abj00918 B Lymphoc
253	61	95.3	14	5	ABJ00919	Abj00919 B Lymphoc
254	61	95.3	14	5	ABJ00917	Abj00917 B Lymphoc
255	61	95.3	14	5	ABJ00921	Abj00921 B Lymphoc
256	61	95.3	14	5	ABJ00923	Abj00923 B Lymphoc
257	61	95.3	14	5	ABJ00924	Abj00924 B Lymphoc
258	61	95.3	14	5	ABJ00920	Abj00920 B Lymphoc
259	61	95.3	14	5	ABJ00925	Abj00925 B Lymphoc
260	61	95.3	14	5	ABJ00922	Abj00922 B Lymphoc
261	61	95.3	14	5	ABG33781	Abg33781 B Lymphoc
262	61	95.3	14	5	ABG33778	Abg33778 B Lymphoc
263	61	95.3	14	5	ABG33780	Abg33780 B Lymphoc
264	61	95.3	14	5	ABG33782	Abg33782 B Lymphoc
265	61	95.3	14	5	ABG33785	Abg33785 B Lymphoc
266	61	95.3	14	5	ABG33784	Abg33784 B Lymphoc
267	61	95.3	14	5	ABG33779	Abg33779 B Lymphoc
268	61	95.3	14	5	ABG33777	Abg33777 B Lymphoc
269	61	95.3	14	5	ABG33783	Abg33783 B Lymphoc
270	61	95.3	14	5	ABG33786	Abg33786 B Lymphoc
271	60	93.8	14	5	ABJ00906	Abj00906 B Lymphoc
272	60	93.8	14	5	ABJ00907	Abj00907 B Lymphoc
273	60	93.8	14	5	ABJ00854	Abj00854 B Lymphoc
274	60	93.8	14	5	ABJ00880	Abj00880 B Lymphoc
275	60	93.8	14	5	ABJ00889	Abj00889 B Lymphoc
276	60	93.8	14	5	ABJ00903	Abj00903 B Lymphoc
277	60	93.8	14	5	ABJ00849	Abj00849 B Lymphoc
278	60	93.8	14	5	ABJ00894	Abj00894 B Lymphoc
279	60	93.8	14	5	ABJ00861	Abj00861 B Lymphoc
280	60	93.8	14	5	ABJ00909	Abj00909 B Lymphoc
281	60	93.8	14	5	ABJ00863	Abj00863 B Lymphoc
282	60	93.8	14	5	ABJ00886	Abj00886 B Lymphoc
283	60	93.8	14	5	ABJ00897	Abj00897 B Lymphoc
284	60	93.8	14	5	ABJ00912	Abj00912 B Lymphoc
285	60	93.8	14	5	ABJ00862	Abj00862 B Lymphoc
286	60	93.8	14	5	ABJ00905	Abj00905 B Lymphoc
287	60	93.8	14	5	ABJ00847	Abj00847 B Lymphoc
288	60	93.8	14	5	ABJ00851	Abj00851 B Lymphoc
289	60	93.8	14	5	ABJ00858	Abj00858 B Lymphoc
290	60	93.8	14	5	ABJ00910	Abj00910 B Lymphoc
291	60	93.8	14	5	ABJ00855	Abj00855 B Lymphoc
292	60	93.8	14	5	ABJ00895	Abj00895 B Lymphoc
293	60	93.8	14	5	ABJ00898	Abj00898 B Lymphoc
294	60	93.8	14	5	ABJ00908	Abj00908 B Lymphoc
295	60	93.8	14	5	ABJ00915	Abj00915 B Lymphoc
296	60	93.8	14	5	ABJ00853	Abj00853 B Lymphoc
297	60	93.8	14	5	ABJ00900	Abj00900 B Lymphoc
298	60	93.8	14	5	ABJ00904	Abj00904 B Lymphoc
299	60	93.8	14	5	ABJ00911	Abj00911 B Lymphoc
300	60	93.8	14	5	ABJ00850	Abj00850 B Lymphoc

## ALIGNMENTS

RESULT 1  
ABJ00997  
ID ABJ00997 standard; peptide; 10 AA.  
XX  
XX ABJ00997;  
XX  
DT 05-SEP-2002 (first entry)  
XX  
DE B lymphocyte stimulator protein binding peptide #168.  
XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;

KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antichititic;  
KW neutropenic; cyclostatic; immunostimulant; antitumor; anti-HIV;  
KW antiaesthetic; antiallergic; thymometric; antianemic; haemostatic;  
KW dermatological; antineoplastic; cardiac; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
OS Unidentified.  
PN WO200216411-A2.  
PD 28-FEB-2002.  
PF 17-AUG-2001; 2001WO-US025850.  
PR 18-AUG-2000; 2000US-0226700P.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PI Belzler JP, Potter DM, Fleming TL, Rosen CA;  
DR WPI; 2002-499775/53.  
PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.  
PS Claim 71; Page 236; 387pp; English.  
XX The present invention relates to the treatment, prevention or  
XX amelioration of a disease or disorder associated with aberrant B  
XX lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells  
XX of haematopoietic origin; or proliferative disease; and reducing,  
XX inhibiting or stimulating immunoglobulin production, B cell proliferation  
XX and graft rejection involving administration of BlyS binding polypeptide.  
XX The BlyS binding polypeptides are used in the treatment, prevention or  
XX amelioration of diseases such as immune system diseases, proliferative  
XX diseases, diseases of cells of hematopoietic origin, graft rejection,  
XX allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
XX hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
XX neurodegenerative diseases. The present sequence is a B lymphocyte  
XX stimulator protein binding peptide  
SQ Sequence 10 AA;  
Query Match 100.0%; Score 64; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00066;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WYDPLTKLML 10  
Db 1 WYDPLTKLML 10  
RESULT 2  
ABJ00977  
ID ABJ00977 standard; peptide; 10 AA.  
XX  
XX ABJ00977;  
XX  
DT 05-SEP-2002 (first entry)  
XX  
DE B lymphocyte affinity maturation library core peptide.  
KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antichititic;  
KW neutropenic; cyclostatic; immunostimulant; antitumor; anti-HIV;  
KW antiaesthetic; antiallergic; thymometric; antianemic; haemostatic;  
KW dermatological; antineoplastic; cardiac; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.

XX Unidentified.  
OS  
XX  
XX WO200216411-A2.  
PN  
XX  
PD 28-FEB-2002.  
XX  
XX 17-AUG-2001; 2001WO-US025850.  
PF  
XX  
PR 18-AUG-2000; 2000US-0226700P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX  
PI Belzter JP, Potter DM, Fleming TL, Rosen CA;  
XX  
XX WPI; 2002-499775/53.  
DR  
XX  
PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.  
XX  
XX Example 11; Page 377; 387pp; English.  
PS  
XX The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of Blys binding polypeptide.  
CC The Blys binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
SQ Sequence 10 AA;  
XX  
Query Match 100.0%; Score 64; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00066;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WYDPLTKLWL 10  
DB 1 WYDPLTKLWL 10  
XX  
RESULT 3  
ABG33859  
ID ABG33859 standard; peptide; 10 AA.  
XX  
AC ABG33859;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE B lymphocyte stimulator (Blys) binding peptide #433.  
XX  
KM B lymphocyte stimulator protein; B lymphocyte stimulator binding peptide;  
KM Blys; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;  
KM synovial fluid; saliva; mucus.  
XX  
OS Synthetic.  
XX  
XX WO200216412-A2.  
PN  
XX  
PD 28-FEB-2002.  
XX  
PF 17-AUG-2001; 2001WO-US025891.  
XX  
PR 18-AUG-2000; 2000US-0226489P.  
XX  
PA (DYAX-) DYAX CORP.  
XX

PI Belzter JP, Potter MD, Fleming TU, Ladner RC;  
XX  
XX WPI; 2002-351647/38.  
DR  
XX  
PT New B-lymphocyte stimulator binding polypeptide useful in detecting or  
PT isolating Blys or Blys-like polypeptide comprises a specified amino acid  
XX sequence.  
XX  
PS Claim 8; Page 98; 269pp; English.  
XX  
XX The invention relates to a B lymphocyte stimulator (Blys) binding  
CC polypeptide. Blys binding peptides bind Blys or Blys-like proteins  
CC reversibly or irreversibly. The binding peptides are used in detection,  
CC isolation and/or purification of Blys in a solution such as water or a  
CC buffer solution, as well as any fluid and/or cell obtained from an  
CC individual biological fluid, body tissue, body cell, cell line, tissue  
CC culture or other source containing Blys or Blys-like polypeptides. The  
CC biological fluid include sera, plasma, lymph, blood, blood fraction,  
CC urine, synovial fluid, spinal fluid, saliva and mucus. Sequences  
CC ABG33406-33415, ABG33423-33575, ABG33588-33846, ABG33848-33850 and  
CC ABG33852-33862 represent Blys binding peptides of the invention  
XX  
SQ Sequence 10 AA;  
XX  
Query Match 100.0%; Score 64; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00066;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WYDPLTKLWL 10  
DB 1 WYDPLTKLWL 10  
XX  
RESULT 4  
ABG33838  
ID ABG33838 standard; peptide; 10 AA.  
XX  
AC ABG33838;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE B lymphocyte stimulator (Blys) binding peptide #414.  
XX  
KM B lymphocyte stimulator protein; B lymphocyte stimulator binding peptide;  
KM Blys; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;  
KM synovial fluid; saliva; mucus.  
XX  
OS Synthetic.  
XX  
XX WO200216412-A2.  
PN  
XX  
PD 28-FEB-2002.  
XX  
PF 17-AUG-2001; 2001WO-US025891.  
XX  
PR 18-AUG-2000; 2000US-0226489P.  
XX  
PA (DYAX-) DYAX CORP.  
XX  
PI Belzter JP, Potter MD, Fleming TU, Ladner RC;  
XX  
XX WPI; 2002-351647/38.  
DR  
XX  
PT New B-lymphocyte stimulator binding polypeptide useful in detecting or  
PT isolating Blys or Blys-like polypeptide comprises a specified amino acid  
XX sequence.  
XX  
PS Claim 4; Page 97; 269pp; English.  
XX  
XX The invention relates to a B lymphocyte stimulator (Blys) binding  
CC polypeptide. Blys binding peptides bind Blys or Blys-like proteins  
CC reversibly or irreversibly. The binding peptides are used in detection,  
CC isolation and/or purification of Blys in a solution such as water or a

CC buffer solution, as well as any fluid and/or cell obtained from an  
CC individual biological fluid, body tissue, body cell, cell line, tissue  
CC culture or other source containing Blys or Blys-like polypeptides. The  
CC biological fluid include sera, plasma, lymph, blood, blood fraction,  
CC urine, synovial fluid, spinal fluid, saliva and mucous. Sequences  
CC ABG33406-33415, ABG33423-33575, ABG33588-33846, ABG33848-33850 and  
CC ABG33852-33862 represent Blys binding peptides of the invention  
XX  
SQ Sequence 10 AA;  
Query Match 100.0%; Score 64; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00066;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WYDPLTKLML 10  
1 WYDPLTKLML 10  
DB 1 WYDPLTKLML 10  
RESULT 5  
ABJ00996  
ID ABJ00996 standard; peptide; 12 AA.  
XX  
AC ABJ00996;  
XX  
DT 05-SEP-2002 (first entry)  
XX  
DE B lymphocyte stimulator protein binding peptide #167.  
XX  
KW B lymphocyte stimulator protein binding protein; Blys; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
KW antiasthmatic; antiallergic; thymimetic; antianaemic; haemostatic;  
KW dermatological; antiinflammatory; cardiant; ophthalmologically; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
OS Unidentified.  
XX  
PN WO200216411-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 17-AUG-2001; 2001WO-US025850.  
XX  
PR 18-AUG-2000; 2000US-0226700P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
XX  
XX WPI; 2002-499775/53.  
DR  
XX  
PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.  
PS  
XX Claim 71; Page 236; 387pp; English.  
XX  
CC The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of Blys binding polypeptide.  
CC The Blys binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide

XX  
SQ Sequence 12 AA;  
Query Match 100.0%; Score 64; DB 5; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.0008;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WYDPLTKLML 10  
1 WYDPLTKLML 10  
DB 1 WYDPLTKLML 10  
RESULT 6  
ABG33858  
ID ABG33858 standard; peptide; 12 AA.  
XX  
AC ABG33858;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE B lymphocyte stimulator (Blys) binding peptide #432.  
XX  
KW B lymphocyte stimulator protein; B lymphocyte stimulator binding peptide;  
KW Blys; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;  
KW synovial fluid; saliva; mucus.  
XX  
OS Synthetic.  
XX  
PN WO200216412-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 17-AUG-2001; 2001WO-US025891.  
XX  
PR 18-AUG-2000; 2000US-0226489P.  
XX  
PA (DYAX-) DYAX CORP.  
XX  
PI Beltzer JP, Potter MD, Fleming TJ, Ladner RC;  
XX  
XX WPI; 2002-351647/38.  
DR  
XX  
PT New B-lymphocyte stimulator binding polypeptide useful in detecting or  
PT isolating Blys or Blys-like polypeptide comprises a specified amino acid  
PT sequence.  
PS  
XX Claim 8; Page 98; 269pp; English.  
XX  
CC The invention relates to a B lymphocyte stimulator (Blys) binding  
CC polypeptide. Blys binding peptides bind Blys or Blys-like proteins  
CC reversibly or irreversibly. The binding peptides are used in detection,  
CC isolation and/or purification of Blys in a solution such as water or a  
CC buffer solution, as well as any fluid and/or cell obtained from an  
CC individual biological fluid, body tissue, body cell, cell line, tissue  
CC culture or other source containing Blys or Blys-like polypeptides. The  
CC biological fluids include sera, plasma, lymph, blood, blood fraction,  
CC urine, synovial fluid, spinal fluid, saliva and mucous. Sequences  
CC ABG33406-33415, ABG33423-33575, ABG33588-33846, ABG33848-33850 and  
CC ABG33852-33862 represent Blys binding peptides of the invention  
XX  
SQ Sequence 12 AA;  
Query Match 100.0%; Score 64; DB 5; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.0008;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WYDPLTKLML 10  
1 WYDPLTKLML 10  
DB 1 WYDPLTKLML 10  
RESULT 7  
ABJ00980

ID ABJ00980 standard; peptide; 13 AA.  
XX  
XX AC ABJ00980;  
XX  
DT 05-SEP-2002 (first entry)  
XX  
XX  
DE B lymphocyte affinity maturation library peptide#253.  
XX  
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antineutritic; antiarthritic;  
KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;  
KW antiasthmatic; antiallergic; thymometric; antinaemic; haemostatic;  
KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
XX Unidentified.  
OS  
XX WO200216411-A2.  
PN  
XX 28-FEB-2002.  
PD  
XX 17-AUG-2001; 2001WO-US025850.  
PF  
XX 18-AUG-2000; 2000US-0226700P.  
PR  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX Beltzer JP, Potter DM, Fleming TJ, Rosen CA;  
PI WPI; 2002-499775/53.  
DR  
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.  
PS  
XX Example 11; Page 220; 387pp; English.  
XX  
XX The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of Blys binding polypeptide.  
CC The Blys binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of haematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
SQ Sequence 13 AA;  
Query Match 100.0%; Score 64; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.00087;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WYDPLTKLWL 10  
DB 1 WYDPLTKLWL 10  
RESULT 8  
ABG33841  
ID ABG33841 standard; peptide; 13 AA.  
XX  
XX ABG33841;  
AC  
XX  
XX 15-JUL-2002 (first entry)  
DT  
XX  
DE B lymphocyte stimulator (Blys) binding peptide #417.

XX  
XX B lymphocyte stimulator protein; B lymphocyte stimulator binding peptide;  
KW Blys; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;  
KW synovial fluid; saliva; mucus.  
XX  
XX Synthetic.  
OS  
XX WO200216412-A2.  
PN  
XX 28-FEB-2002.  
PD  
XX 17-AUG-2001; 2001WO-US025891.  
PF  
XX 18-AUG-2000; 2000US-0226489P.  
PR  
XX (DYAX-) DYAX CORP.  
PA  
XX Beltzer JP, Potter MD, Fleming TJ, Ladner RC;  
PI WPI; 2002-351647/38.  
DR  
XX  
XX New B-lymphocyte stimulator binding polypeptide useful in detecting or  
PT isolating Blys or Blys-like polypeptide comprises a specified amino acid  
PS sequence.  
XX  
XX Claim 7; Page 94; 269pp; English.  
XX  
XX The invention relates to a B lymphocyte stimulator (Blys) binding  
CC polypeptide. Blys binding peptides bind Blys or Blys-like proteins  
CC reversibly or irreversibly. The binding peptides are used in detection,  
CC isolation and/or purification of Blys in a solution such as water or a  
CC buffer solution, as well as any fluid and/or cell obtained from an  
CC individual biological fluid, body tissue, body cell, cell line, tissue  
CC culture or other source containing Blys or Blys-like polypeptides. The  
CC biological fluids include sera, plasma, lymph, blood, blood fraction,  
CC urine, synovial fluid, spinal fluid, saliva and mucus. Sequences  
CC ABG33406-33415, ABG33423-33575, ABG33588-33846, ABG33848-33850 and  
CC ABG33852-33862 represent Blys binding peptides of the invention  
XX  
SQ Sequence 13 AA;  
Query Match 100.0%; Score 64; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.00087;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WYDPLTKLWL 10  
DB 1 WYDPLTKLWL 10  
RESULT 9  
ABJ00739  
ID ABJ00739 standard; peptide; 14 AA.  
XX  
XX ABJ00739;  
AC  
XX  
XX 05-SEP-2002 (first entry)  
DT  
XX  
XX B lymphocyte affinity maturation library peptide #13.  
DE  
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antineutritic; antiarthritic;  
KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;  
KW antiasthmatic; antiallergic; thymometric; antinaemic; haemostatic;  
KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
XX Unidentified.  
OS  
XX WO200216411-A2.  
PN

XX 28-FEB-2002.  
XX 17-AUG-2001; 2001WO-US025850.  
XX 18-AUG-2000; 2000US-0226700P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Belzter JP, Potter DM, Fleming TL, Rosen CA;  
XX WPI; 2002-499775/53.  
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises  
XX administering B lymphocyte stimulator binding polypeptide.  
XX Claim 70; Page 214; 387pp; English.  
XX The present invention relates to the treatment, prevention or  
XX amelioration of a disease or disorder associated with aberrant B  
XX lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
XX of haematopoietic origin; or proliferative disease; and reducing,  
XX inhibiting or stimulating immunoglobulin production, B cell proliferation  
XX and graft rejection involving administration of Blys binding polypeptide.  
XX The Blys binding polypeptides are used in the treatment, prevention or  
XX amelioration of diseases such as immune system diseases, proliferative  
XX diseases, diseases of cells of hematopoietic origin, graft rejection,  
XX allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
XX hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
XX neurodegenerative diseases. The present sequence is a B lymphocyte  
XX stimulator protein binding peptide  
XX Sequence 14 AA;  
SQ

Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLML 10  
|||  
3 WYDPLTKLML 12

## RESULT 10

ABJ00744 ID ABJ00744 standard; peptide; 14 AA.

AC ABJ00744;

DT 05-SEP-2002 (first entry)

DE B lymphocyte affinity maturation library peptide #18.

XX B lymphocyte stimulator protein binding protein; Blys; immune disease;  
XX allergy; proliferative disease; infectious disease; arteriosclerosis;  
XX inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
XX ischaemia; graft-versus-host disease; neurodegenerative disease;  
XX immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
XX neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
XX antiaesthetic; anti-allergic; thymimetic; antianemic; haemostatic;  
XX dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
XX antidiabetic; antithyroid; antidepressant; hepatotropic.

XX Unidentified.

XX WO200216411-A2.

XX 28-FEB-2002.

XX 17-AUG-2001; 2001WO-US025850.

XX 18-AUG-2000; 2000US-0226700P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX Belzter JP, Potter DM, Fleming TL, Rosen CA;

XX WPI; 2002-499775/53.

XX The treatment of various diseases e.g. rheumatoid arthritis, comprises  
XX administering B lymphocyte stimulator binding polypeptide.

XX Claim 70; Page 214; 387pp; English.

XX The present invention relates to the treatment, prevention or  
XX amelioration of a disease or disorder associated with aberrant B  
XX lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
XX of haematopoietic origin; or proliferative disease; and reducing,  
XX inhibiting or stimulating immunoglobulin production, B cell proliferation  
XX and graft rejection involving administration of Blys binding polypeptide.  
XX The Blys binding polypeptides are used in the treatment, prevention or  
XX amelioration of diseases such as immune system diseases, proliferative  
XX diseases, diseases of cells of hematopoietic origin, graft rejection,  
XX allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
XX hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
XX neurodegenerative diseases. The present sequence is a B lymphocyte  
XX stimulator protein binding peptide  
XX Sequence 14 AA;  
SQ

Query Match. 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLML 10  
|||  
3 WYDPLTKLML 12

## RESULT 11

ABJ00770 ID ABJ00770 standard; peptide; 14 AA.

AC ABJ00770;

DT 05-SEP-2002 (first entry)

DE B lymphocyte affinity maturation library peptide #44.

XX B lymphocyte stimulator protein binding protein; Blys; immune disease;  
XX allergy; proliferative disease; infectious disease; arteriosclerosis;  
XX inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
XX ischaemia; graft-versus-host disease; neurodegenerative disease;  
XX immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
XX neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
XX antiaesthetic; anti-allergic; thymimetic; antianemic; haemostatic;  
XX dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
XX antidiabetic; antithyroid; antidepressant; hepatotropic.

XX Unidentified.

XX WO200216411-A2.

XX 28-FEB-2002.

XX 17-AUG-2001; 2001WO-US025850.

XX 18-AUG-2000; 2000US-0226700P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Belzter JP, Potter DM, Fleming TL, Rosen CA;

XX WPI; 2002-499775/53.

XX The treatment of various diseases e.g. rheumatoid arthritis, comprises

[illegible]

CC	of haematopoietic origin; or proliferative disease; and reducing,
CC	inhibiting or stimulating immunoglobulin production, B cell proliferation
CC	and graft rejection involving administration of Blys binding polypeptide.
CC	The Blys binding polypeptides are used in the treatment, prevention or
CC	amelioration of diseases such as immune system diseases, proliferative
CC	diseases, diseases of cells of hematopoietic origin, graft rejection,
CC	allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC	hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC	neurodegenerative diseases. The present sequence is a B lymphocyte
CC	stimulator protein binding peptide
SQ	Sequence 14 AA;
Dn	3 WYDPLTKLML 12
Oy	1 WYDPLTKLML 10       
Db	3 WYDPLTKLML 12
RESULT 13	
ID	ABJ00793 standard; peptide; 14 AA.
XX	ABJ00793
AC	ABJ00793;
XX	
DT	05-SEP-2002 (first entry)
DE	B lymphocyte affinity maturation library peptide #67.
XX	
KW	B lymphocyte stimulator protein binding protein; Blys; immune disease;
KW	allergy; proliferative disease; infectious disease; arteriosclerosis;
KW	inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KM	ischaemia; graft-versus-host disease; neurodegenerative disease;
KW	immunosuppressive; nephrotropic; antineumatic; antiarthritic;
KW	neuroprotective; cytostatic; immunostimulant; antitumor; anti-HIV;
KW	antiaesthetic; anti-allergic; thymometric; antinaemic; haemostatic;
KW	dematological; anti-inflammatory; cardiac; ophthalmological; uropathic;
XX	antidiabetic; antichryoid; antidepressant; hepatotropic.
OS	Unidentified.
PN	WO200216411-A2.
PD	28-FEB-2002.
PF	17-AUG-2001; 2001WO-US025850.
PR	18-AUG-2000; 2000US-0226700P.
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
I1	Beltzer JP, Potter DM, Fleming TL, Rosen CA;
DR	WPI; 2002-499775/53.
PT	The treatment of various diseases e.g. rheumatoid arthritis, comprises
PTe	administering B lymphocyte stimulator binding polypeptide.
PS	Claim 70; Page 215; 387pp; English.
XX	
CC	The present invention relates to the treatment, prevention or
CC	amelioration of a disease or disorder associated with: aberrant B
CC	lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
CC	of haematopoietic origin; or proliferative disease; and reducing,
CC	inhibiting or stimulating immunoglobulin production, B cell proliferation
CC	and graft rejection involving administration of Blys binding polypeptide.
CC	The Blys binding polypeptides are used in the treatment, prevention or
CC	amelioration of diseases such as immune system diseases, proliferative
CC	diseases, diseases of cells of hematopoietic origin, graft rejection,
CC	allergies, infectious diseases, arteriosclerosis, inflammatory disorders,



CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
XX

SO Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLWL 10  
|||  
DB 3 WYDPLTKLWL 12

RESULT 14  
ABJ00818  
ID ABJ00818 standard; peptide; 14 AA.  
XX  
XX

AC ABJ00818;  
XX  
XX 05-SEP-2002. (first entry)

DE B lymphocyte affinity maturation library peptide #92.

XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
KW antiaesthetic; antiallergic; thymomimetic; antanaemic; haemostatic;  
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.

XX Unidentified.

OS  
XX WO200216411-A2.

PN 28-FEB-2002.

PD 17-AUG-2001; 2001WO-US025850.

PF 18-AUG-2000; 2000US-0226700P.

PR (HUMA-) HUMAN GENOME SCI INC.

XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;

PI  
XX WPI, 2002-499775/53.

DR The treatment of various diseases e.g. rheumatoid arthritis, comprises  
XX administering B lymphocyte stimulator binding polypeptide.  
PT

PS Claim 70; Page 215; 387pp; English.

XX The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of BlyS binding polypeptide.  
CC The BlyS binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of haematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX

SO Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLWL 10  
|||  
DB 3 WYDPLTKLWL 12

RESULT 15  
ABJ00826  
ID ABJ00826 standard; peptide; 14 AA.  
XX  
XX

AC ABJ00826;

XX 05-SEP-2002. (first entry)

DE B lymphocyte affinity maturation library peptide #100.

XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
KW antiaesthetic; antiallergic; thymomimetic; antanaemic; haemostatic;  
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.

XX Unidentified.

OS  
XX WO200216411-A2.

PN 28-FEB-2002.

PD 17-AUG-2001; 2001WO-US025850.

PF 18-AUG-2000; 2000US-0226700P.

PR (HUMA-) HUMAN GENOME SCI INC.

XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;

PI  
XX WPI, 2002-499775/53.

DR The treatment of various diseases e.g. rheumatoid arthritis, comprises  
XX administering B lymphocyte stimulator binding polypeptide.  
PT

PS Claim 70; Page 216; 387pp; English.

XX The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of BlyS binding polypeptide.  
CC The BlyS binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of haematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX

SO Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLWL 10  
|||  
DB 3 WYDPLTKLWL 12

RESULT 16  
 ID ABJ00836 standard; peptide; 14 AA.  
 XX  
 AC ABJ00836;  
 XX  
 DT 05-SEP-2002 (first entry)  
 XX  
 DE B lymphocyte affinity maturation library peptide #110.  
 XX  
 KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
 KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
 KW antiasthmatic; antiallergic; thyromimetic; antianaemic; haemostatic;  
 KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200216411-A2.  
 XX  
 PD 28-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-US025850.  
 XX  
 PR 18-AUG-2000; 2000US-0226700P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Belzter JP, Potter DM, Fleming TL, Rosen CA;  
 XX  
 DR WPI; 2002-499775/53.  
 XX  
 PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
 PT administering B lymphocyte stimulator binding polypeptide.  
 XX  
 PS Claim 70; Page 216; 387pp; English.  
 XX  
 CC The present invention relates to the treatment, prevention or  
 CC amelioration of a disease or disorder associated with: aberrant B  
 CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells  
 CC of haematopoietic origin; or proliferative disease; and reducing,  
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
 CC and graft rejection involving administration of BlyS binding polypeptide.  
 CC The BlyS binding polypeptides are used in the treatment, prevention or  
 CC amelioration of diseases such as immune system diseases, proliferative  
 CC diseases, diseases of cells of haematopoietic origin, graft rejection,  
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
 CC neurodegenerative diseases. The present sequence is a B lymphocyte  
 CC stimulator protein binding peptide  
 XX  
 SQ Sequence 14 AA;  
 XX  
 Query Match 100.0%; Score 64; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.00094;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 WYDPLTKLML 10  
 |||||  
 DB 3 WYDPLTKLML 12  
 |||||  
 RESULT 17  
 ID ABJ00794 standard; peptide; 14 AA.  
 XX  
 AC ABJ00794;  
 XX  
 DT 05-SEP-2002 (first entry)  
 XX  
 DE B lymphocyte affinity maturation library peptide #95.  
 XX  
 KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
 KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
 KW antiasthmatic; antiallergic; thyromimetic; antianaemic; haemostatic;  
 KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.

DT 05-SEP-2002 (first entry)  
 XX  
 DE B lymphocyte affinity maturation library peptide #68.  
 XX  
 KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
 KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
 KW antiasthmatic; antiallergic; thyromimetic; antianaemic; haemostatic;  
 KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200216411-A2.  
 XX  
 PD 28-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-US025850.  
 XX  
 PR 18-AUG-2000; 2000US-0226700P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Belzter JP, Potter DM, Fleming TL, Rosen CA;  
 XX  
 DR WPI; 2002-499775/53.  
 XX  
 PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
 PT administering B lymphocyte stimulator binding polypeptide.  
 XX  
 PS Claim 70; Page 215; 387pp; English.  
 XX  
 CC The present invention relates to the treatment, prevention or  
 CC amelioration of a disease or disorder associated with: aberrant B  
 CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells  
 CC of haematopoietic origin; or proliferative disease; and reducing,  
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
 CC and graft rejection involving administration of BlyS binding polypeptide.  
 CC The BlyS binding polypeptides are used in the treatment, prevention or  
 CC amelioration of diseases such as immune system diseases, proliferative  
 CC diseases, diseases of cells of haematopoietic origin, graft rejection,  
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
 CC neurodegenerative diseases. The present sequence is a B lymphocyte  
 CC stimulator protein binding peptide  
 XX  
 SQ Sequence 14 AA;  
 XX  
 Query Match 100.0%; Score 64; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.00094;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 WYDPLTKLML 10  
 |||||  
 DB 3 WYDPLTKLML 12  
 |||||  
 RESULT 18  
 ID ABJ00821 standard; peptide; 14 AA.  
 XX  
 AC ABJ00821;  
 XX  
 DT 05-SEP-2002 (first entry)  
 XX  
 DE B lymphocyte affinity maturation library peptide #95.  
 XX  
 KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
 KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
 KW antiasthmatic; antiallergic; thyromimetic; antianaemic; haemostatic;  
 KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.

ischaemia; graft-versus-host disease; neurodegenerative disease;  
immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
neuroprotective; cytostatic; immunostimulant; antitumor; anti-HIV;  
antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;  
dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
antidiabetic; antithyroid; antidepressant; hepatotropic;  
OS Unidentified.  
XX  
XX WO200216411-A2.  
XX  
XX 28-FEB-2002.  
XX  
XX 17-AUG-2001; 2001WO-US025850.  
XX  
XX 18-AUG-2000; 2000US-0226700P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Belzer JP, Potter DM, Fleming TL, Rosen CA;  
XX  
XX WPI; 2002-499775/53.  
XX  
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises  
XX administering B lymphocyte stimulator binding polypeptide.  
XX  
XX Claim 70; Page 216; 387pp; English.  
XX  
XX The present invention relates to the treatment, prevention or  
XX amelioration of a disease or disorder associated with: aberrant B  
XX lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
XX of haematopoietic origin; or proliferative disease; and reducing,  
XX inhibiting or stimulating immunoglobulin production, B cell proliferation  
XX and graft rejection involving administration of Blys binding polypeptide.  
XX The Blys binding polypeptides are used in the treatment, prevention or  
XX amelioration of diseases such as immune system diseases, proliferative  
XX diseases, diseases of cells of hematopoietic origin, graft rejection,  
XX allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
XX hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
XX neurodegenerative diseases. The present sequence is a B lymphocyte  
XX stimulator protein binding peptide  
XX  
SQ Sequence 14 AA;  
  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 WYDPLTKLML 10  
|||  
3 WYDPLTKLML 12  
DB  
  
RESULT 19  
ABJ00832  
ID ABJ00832 standard; peptide; 14 AA.  
XX  
XX ABJ00832;  
AC  
XX  
DT 05-SEP-2002 (first entry)  
XX  
XX B lymphocyte affinity maturation library peptide #106.  
DE  
XX B lymphocyte stimulator protein binding protein, Blys; immune disease;  
XX allergy; proliferative disease; infectious disease; arteriosclerosis;  
XX inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
XX ischaemia; graft-versus-host disease; neurodegenerative disease;  
XX immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
XX neuroprotective; cytostatic; immunostimulant; antitumor; anti-HIV;  
XX antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;  
XX dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
XX antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX

Unidentified.  
OS  
XX  
XX WO200216411-A2.  
XX  
XX 28-FEB-2002.  
XX  
XX 17-AUG-2001; 2001WO-US025850.  
XX  
XX 18-AUG-2000; 2000US-0226700P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Belzer JP, Potter DM, Fleming TL, Rosen CA;  
XX  
XX WPI; 2002-499775/53.  
XX  
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises  
XX administering B lymphocyte stimulator binding polypeptide.  
XX  
XX Claim 70; Page 216; 387pp; English.  
XX  
XX The present invention relates to the treatment, prevention or  
XX amelioration of a disease or disorder associated with: aberrant B  
XX lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
XX of haematopoietic origin; or proliferative disease; and reducing,  
XX inhibiting or stimulating immunoglobulin production, B cell proliferation  
XX and graft rejection involving administration of Blys binding polypeptide.  
XX The Blys binding polypeptides are used in the treatment, prevention or  
XX amelioration of diseases such as immune system diseases, proliferative  
XX diseases, diseases of cells of hematopoietic origin, graft rejection,  
XX allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
XX hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
XX neurodegenerative diseases. The present sequence is a B lymphocyte  
XX stimulator protein binding peptide  
XX  
SQ Sequence 14 AA;  
  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 WYDPLTKLML 10  
|||  
3 WYDPLTKLML 12  
DB  
  
RESULT 20  
ABJ00731  
ID ABJ00731 standard; peptide; 14 AA.  
XX  
XX ABJ00731;  
AC  
XX  
DT 05-SEP-2002 (first entry)  
XX  
XX B lymphocyte affinity maturation library peptide #5.  
DE  
XX B lymphocyte stimulator protein binding protein, Blys; immune disease;  
XX allergy; proliferative disease; infectious disease; arteriosclerosis;  
XX inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
XX ischaemia; graft-versus-host disease; neurodegenerative disease;  
XX immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
XX neuroprotective; cytostatic; immunostimulant; antitumor; anti-HIV;  
XX antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;  
XX dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
XX antidiabetic; antithyroid; antidepressant; hepatotropic.  
OS  
XX  
XX Unidentified.  
XX  
XX WO200216411-A2.  
XX  
XX 28-FEB-2002.  
XX  
XX 17-AUG-2001; 2001WO-US025850.  
XX

XX 18-AUG-2000; 2000US-0226700P.  
 PR (HUMA-) HUMAN GENOME SCT INC.  
 XX  
 PA Beltzner JP, Potter DM, Fleming TL, Rosen CA;  
 PI  
 XX WPI; 2002-499775/53.  
 DR  
 XX The treatment of various diseases e.g. rheumatoid arthritis, comprises  
 PT administering B lymphocyte stimulator binding polypeptide.  
 XX  
 PS Claim 70; Page 214; 387pp; English.  
 XX  
 CC The present invention relates to the treatment, prevention or  
 CC amelioration of a disease or disorder associated with: aberrant B  
 CC lymphocyte stimulator (BLyS), BLyS receptor expression or activity; cells  
 CC of haematopoietic origin; or proliferative disease; and reducing, cells  
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
 CC and graft rejection involving administration of BLyS binding polypeptide.  
 CC The BLyS binding polypeptides are used in the treatment, prevention or  
 CC amelioration of diseases such as immune system diseases, proliferative  
 CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
 CC neurodegenerative diseases. The present sequence is a B lymphocyte  
 CC stimulator protein binding peptide  
 XX  
 SQ Sequence 14 AA;  
 XX  
 Query Match 100.0%; Score 64; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.00094;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 WYDPLTKLWL 10  
 DB 3 WYDPLTKLWL 12  
 XX  
 RESULT 21  
 ABJ00773  
 ID ABJ00773 standard; peptide; 14 AA.  
 AC ABJ00773;  
 XX  
 DT 05-SEP-2002 (first entry)  
 XX  
 DE B lymphocyte affinity maturation library peptide #47.  
 XX  
 KW B lymphocyte stimulator protein binding protein; BLyS; immune disease;  
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
 KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;  
 KW antiasthmatic; anti-allergic; thymostimulant; antianaemic; haemostatic;  
 KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200216411-A2.  
 XX  
 PD 28-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-US025850.  
 XX  
 PR 18-AUG-2000; 2000US-0226700P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCT INC.  
 XX  
 PI Beltzner JP, Potter DM, Fleming TL, Rosen CA;  
 XX

DR WPI; 2002-499775/53.  
 XX  
 XX The treatment of various diseases e.g. rheumatoid arthritis, comprises  
 PT administering B lymphocyte stimulator binding polypeptide.  
 XX  
 PS Claim 70; Page 215; 387pp; English.  
 XX  
 CC The present invention relates to the treatment, prevention or  
 CC amelioration of a disease or disorder associated with: aberrant B  
 CC lymphocyte stimulator (BLyS), BLyS receptor expression or activity; cells  
 CC of haematopoietic origin; or proliferative disease; and reducing, cells  
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
 CC and graft rejection involving administration of BLyS binding polypeptide.  
 CC The BLyS binding polypeptides are used in the treatment, prevention or  
 CC amelioration of diseases such as immune system diseases, proliferative  
 CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
 CC neurodegenerative diseases. The present sequence is a B lymphocyte  
 CC stimulator protein binding peptide  
 XX  
 SQ Sequence 14 AA;  
 XX  
 Query Match 100.0%; Score 64; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.00094;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 WYDPLTKLWL 10  
 DB 3 WYDPLTKLWL 12  
 XX  
 RESULT 22  
 ABJ00809  
 ID ABJ00809 standard; peptide; 14 AA.  
 AC ABJ00809;  
 XX  
 DT 05-SEP-2002 (first entry)  
 XX  
 DE B lymphocyte affinity maturation library peptide #83.  
 XX  
 KW B lymphocyte stimulator protein binding protein; BLyS; immune disease;  
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
 KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;  
 KW antiasthmatic; anti-allergic; thymostimulant; antianaemic; haemostatic;  
 KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200216411-A2.  
 XX  
 PD 28-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-US025850.  
 XX  
 PR 18-AUG-2000; 2000US-0226700P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCT INC.  
 XX  
 PI Beltzner JP, Potter DM, Fleming TL, Rosen CA;  
 XX  
 DR WPI; 2002-499775/53.  
 XX  
 XX The treatment of various diseases e.g. rheumatoid arthritis, comprises  
 PT administering B lymphocyte stimulator binding polypeptide.  
 XX  
 PS Claim 70; Page 215; 387pp; English.  
 XX

CC The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of Blys binding polypeptide.  
CC The Blys binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide

SO Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10  
|||  
3 WYDPLTKLWL 12

Db 3 WYDPLTKLWL 12

RESULT 23  
ABJ00816  
ID ABJ00816 standard; peptide; 14 AA.  
AC ABJ00816;  
XX  
XX 05-SEP-2002 (first entry)  
DT  
XX  
XX B lymphocyte affinity maturation library peptide #90.  
DE  
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neuroprotective; cyostatic; immunostimulant; antitumor; anti-HIV;  
KW antiaesthetic; antiallergic; thymostimetic; antianemic; haemostatic;  
KW dermatologic; antiinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
KM  
XX  
XX unidentified.  
OS  
XX  
XX WO200216411-A2.  
FN  
XX  
XX 28-FEB-2002.  
PD  
XX  
XX 17-AUG-2001; 2001WO-US025850.  
PF  
XX  
XX 18-AUG-2000; 2000US-0226700P.  
PR  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX  
XX Belzter JP, Potter DM, Fleming TL, Rosen CA;  
PI  
XX  
XX WPI; 2002-499775/53.  
DR  
XX  
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.  
PT  
XX  
XX Claim 70; Page 215; 387pp; English.  
PS  
XX  
XX The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of Blys binding polypeptide.  
CC The Blys binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide

CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide

SO Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10  
|||  
3 WYDPLTKLWL 12

Db 3 WYDPLTKLWL 12

RESULT 24  
ABJ00822  
ID ABJ00822 standard; peptide; 14 AA.  
AC ABJ00822;  
XX  
XX 05-SEP-2002 (first entry)  
DT  
XX  
XX B lymphocyte affinity maturation library peptide #96.  
DE  
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neuroprotective; cyostatic; immunostimulant; antitumor; anti-HIV;  
KW antiaesthetic; antiallergic; thymostimetic; antianemic; haemostatic;  
KW dermatologic; antiinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
KM  
XX  
XX unidentified.  
OS  
XX  
XX WO200216411-A2.  
FN  
XX  
XX 28-FEB-2002.  
PD  
XX  
XX 17-AUG-2001; 2001WO-US025850.  
PF  
XX  
XX 18-AUG-2000; 2000US-0226700P.  
PR  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX  
XX Belzter JP, Potter DM, Fleming TL, Rosen CA;  
PI  
XX  
XX WPI; 2002-499775/53.  
DR  
XX  
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.  
PT  
XX  
XX Claim 70; Page 216; 387pp; English.  
PS  
XX  
XX The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of Blys binding polypeptide.  
CC The Blys binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide

SQ Sequence 14 AA;  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WYDPLTKLML 10  
|||||  
3 WYDPLTKLML 12  
DB 3 WYDPLTKLML 12  
RESULT 25  
ABJ00830  
ID ABJ00830 standard; peptide; 14 AA.  
XX  
AC ABJ00830;  
XX  
DT 05-SEP-2002 (first entry)  
XX  
DE B lymphocyte affinity maturation library peptide #104.  
XX  
KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antineumatic; antitumour; anti-HIV;  
KW neuroprotective; cyostatic; immunostimulant; antiaesthetic;  
KW antisthmatic; antiallergic; thyromimetic; antinaemic; haemostatic;  
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
OS Unidentified.  
XX  
PN WO200216411-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 17-AUG-2001; 2001WO-US025850.  
XX  
PR 18-AUG-2000; 2000US-0226700P.  
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PS (HUMA-) HUMAN GENOME SCI INC.  
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PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
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DR WPI; 2002-499775/53.  
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CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing, cells  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of BlyS binding polypeptide.  
CC The BlyS binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of haematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
SQ Sequence 14 AA;  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WYDPLTKLML 10  
|||||  
3 WYDPLTKLML 12  
DB 3 WYDPLTKLML 12  
RESULT 27  
ABJ00730  
ID ABJ00730 standard; peptide; 14 AA.

DB 3 WYDPLTKLML 12  
RESULT 26  
ABJ00831  
ID ABJ00831 standard; peptide; 14 AA.  
XX  
AC ABJ00831;  
XX  
DT 05-SEP-2002 (first entry)  
XX  
DE B lymphocyte affinity maturation library peptide #105.  
XX  
KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antineumatic; antitumour; anti-HIV;  
KW neuroprotective; cyostatic; immunostimulant; antiaesthetic;  
KW antisthmatic; antiallergic; thyromimetic; antinaemic; haemostatic;  
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
OS Unidentified.  
XX  
PN WO200216411-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 17-AUG-2001; 2001WO-US025850.  
XX  
PR 18-AUG-2000; 2000US-0226700P.  
XX  
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PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
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DR WPI; 2002-499775/53.  
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CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of BlyS binding polypeptide.  
CC The BlyS binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of haematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
SQ Sequence 14 AA;  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WYDPLTKLML 10  
|||||  
3 WYDPLTKLML 12  
DB 3 WYDPLTKLML 12  
RESULT 27  
ABJ00730  
ID ABJ00730 standard; peptide; 14 AA.

XX AC ABJ00730;  
XX DT 05-SEP-2002 (first entry)  
XX DE B lymphocyte affinity maturation library peptide #4.  
XX KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neuromuscular; cytosolic; immunostimulant; antitumour; anti-HIV;  
KW antiaesthetic; antiallergic; thymimetic; antineoplastic; haemostatic;  
KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX OS Unidentified.  
XX PN WO200216411-A2.  
XX PD 28-FEB-2002.  
XX PF 17-AUG-2001; 2001WO-US025850.  
XX PR 18-AUG-2000; 2000US-0226700P.  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
XX DR WPI; 2002-499775/53.  
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CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of BlyS binding polypeptide.  
CC The BlyS binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of haematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX SQ Sequence 14 AA;  
XX  
XX Query Match 100.0%; Score 64; DB 5; Length 14;  
XX Best Local Similarity 100.0%; Pred. No. 0.00094;  
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 WYDPLTKML 10  
XX |||||  
XX 3 WYDPLTKML 12  
XX DB  
XX  
XX RESULT 28  
XX ID ABJ00738 standard; peptide; 14 AA.  
XX AC ABJ00738;  
XX DT 05-SEP-2002 (first entry)  
XX DE B lymphocyte affinity maturation library peptide #12.  
XX KW

KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neuromuscular; cytosolic; immunostimulant; antitumour; anti-HIV;  
KW antiaesthetic; antiallergic; thymimetic; antineoplastic; haemostatic;  
KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX OS Unidentified.  
XX PN WO200216411-A2.  
XX PD 28-FEB-2002.  
XX PF 17-AUG-2001; 2001WO-US025850.  
XX PR 18-AUG-2000; 2000US-0226700P.  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
XX DR WPI; 2002-499775/53.  
XX PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
XX PT administering B lymphocyte stimulator binding polypeptide.  
XX PS Claim 70; Page 214; 387pp; English.  
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CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of BlyS binding polypeptide.  
CC The BlyS binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of haematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX SQ Sequence 14 AA;  
XX  
XX Query Match 100.0%; Score 64; DB 5; Length 14;  
XX Best Local Similarity 100.0%; Pred. No. 0.00094;  
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 WYDPLTKML 10  
XX |||||  
XX 3 WYDPLTKML 12  
XX DB  
XX  
XX RESULT 29  
XX ID ABJ00754 standard; peptide; 14 AA.  
XX AC ABJ00754;  
XX DT 05-SEP-2002 (first entry)  
XX DE B lymphocyte affinity maturation library peptide #28.  
XX KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neuromuscular; cytosolic; immunostimulant; antitumour; anti-HIV;  
KW antiaesthetic; antiallergic; thymimetic; antineoplastic; haemostatic;  
KW

KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KM antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX Unidentified.  
OS  
XX WO200216411-A2.  
XX  
XX  
PD 28-FEB-2002.  
XX  
XX 17-AUG-2001; 2001WO-US025850.  
XX  
XX 18-AUG-2000; 2000US-0226700P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
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XX Belzter JP, Potter DM, Fleming TL, Rosen CA;  
PI WPI; 2002-499775/53.  
XX  
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DR The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.  
XX  
XX Claim 70; Page 214; 387pp; English.  
XX  
XX The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (BLyS), BLyS receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of BLyS binding polypeptide.  
CC The BLyS binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
XX  
SQ Sequence 14 AA;  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 WYDPLTKLWL 10  
|||  
3 WYDPLTKLWL 12  
DB  
RESULT 30  
ABJ00777  
ID ABJ00777 standard; peptide; 14 AA.  
XX  
XX ABJ00777;  
AC  
XX  
DT 05-SEP-2002 (first entry)  
XX  
XX B lymphocyte affinity maturation library peptide #51.  
DE  
XX B lymphocyte stimulator protein binding protein; BLyS; immune disease;  
KM allergy; proliferative disease; infectious disease; arteriosclerosis;  
KM inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KM ischaemia; graft-versus-host disease; neurodegenerative disease;  
KM immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KM neutroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
KM antiaschematic; anti-allergic; thyromimetic; antianaemic; haemostatic;  
KM dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KM antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
XX Unidentified.  
OS  
XX  
XX WO200216411-A2.  
XX

PD 28-FEB-2002.  
XX  
XX 17-AUG-2001; 2001WO-US025850.  
XX  
XX 18-AUG-2000; 2000US-0226700P.  
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XX (HUMA-) HUMAN GENOME SCI INC.  
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CC lymphocyte stimulator (BLyS), BLyS receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of BLyS binding polypeptide.  
CC The BLyS binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
XX  
SQ Sequence 14 AA;  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 WYDPLTKLWL 10  
|||  
3 WYDPLTKLWL 12  
DB  
RESULT 31  
ABJ00835  
ID ABJ00835 standard; peptide; 14 AA.  
XX  
XX ABJ00835;  
AC  
XX  
DT 05-SEP-2002 (first entry)  
XX  
XX B lymphocyte affinity maturation library peptide #109.  
DE  
XX B lymphocyte stimulator protein binding protein; BLyS; immune disease;  
KM allergy; proliferative disease; infectious disease; arteriosclerosis;  
KM inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KM ischaemia; graft-versus-host disease; neurodegenerative disease;  
KM immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KM neutroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
KM antiaschematic; anti-allergic; thyromimetic; antianaemic; haemostatic;  
KM dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KM antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
XX Unidentified.  
OS  
XX  
XX WO200216411-A2.  
XX  
XX 28-FEB-2002.  
XX  
XX 17-AUG-2001; 2001WO-US025850.  
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CC and graft rejection involving administration of BlyS binding polypeptide.  
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CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX SQ Sequence 14 AA;  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WYDPLTKLWL 10  
Db 3 WYDPLTKLWL 12  
RESULT 32  
ABJ00771 standard; peptide; 14 AA.  
XX AC ABJ00771;  
XX DT 05-SEP-2002 (first entry)  
XX B lymphocyte affinity maturation library peptide #45.  
XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neutroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;  
KW antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;  
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX OS Unidentified.  
XX WO200216411-A2.  
XX 28-FEB-2002.  
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XX 18-AUG-2000; 2000US-0226700P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
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CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX SQ Sequence 14 AA;  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WYDPLTKLWL 10  
Db 3 WYDPLTKLWL 12  
RESULT 33  
ABJ00798 standard; peptide; 14 AA.  
XX AC ABJ00798;  
XX DT 05-SEP-2002 (first entry)  
XX B lymphocyte affinity maturation library peptide #72.  
XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neutroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;  
KW antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;  
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX OS Unidentified.  
XX WO200216411-A2.  
XX 28-FEB-2002.  
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XX 18-AUG-2000; 2000US-0226700P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
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CC hypergammaglobulinemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
SQ Sequence 14 AA;  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WYDPLTKLML 10  
DB 3 WYDPLTKLML 12  
RESULT 34  
ID ABJ00803 standard; peptide; 14 AA.  
XX  
AC ABJ00803;  
XX  
DT 05-SEP-2002 (first entry)  
XX  
DE B lymphocyte affinity maturation library peptide #77.  
XX  
KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antineumatic; antiarthritic;  
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
KW antidiabetic; antiallergic; thyromimetic; antinaemic; haemostatic;  
KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
OS Unidentified.  
XX  
PN WO200216411-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 17-AUG-2001; 2001WO-US025850.  
XX  
PR 18-AUG-2000; 2000US-0226700P.  
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PI WPI; 2002-499775/53.  
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CC amelioration of a disease or disorder associated with: aberrant B  
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CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of BlyS binding polypeptide.  
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CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
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CC hypergammaglobulinemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
SQ Sequence 14 AA;  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
SQ Sequence 14 AA;  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WYDPLTKLML 10  
DB 3 WYDPLTKLML 12  
RESULT 35  
ID ABJ00827 standard; peptide; 14 AA.  
XX  
AC ABJ00827;  
XX  
DT 05-SEP-2002 (first entry)  
XX  
DE B lymphocyte affinity maturation library peptide #101.  
XX  
KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antineumatic; antiarthritic;  
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
KW antidiabetic; antiallergic; thyromimetic; antinaemic; haemostatic;  
KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
OS Unidentified.  
XX  
PN WO200216411-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 17-AUG-2001; 2001WO-US025850.  
XX  
PR 18-AUG-2000; 2000US-0226700P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
XX  
PI WPI; 2002-499775/53.  
XX  
PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.  
XX  
XX Claim 70; Page 216; 387pp; English.  
XX  
CC The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of BlyS binding polypeptide.  
CC The BlyS binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
SQ Sequence 14 AA;  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLWL 10  
| | | | | | | | | |  
| | | | | | | | | |

Db 3 WYDPLTKLWL 12

## RESULT 36

ABJ00833

ID ABJ00833 standard; peptide; 14 AA.

AC ABJ00833;

DT 05-SEP-2002 (first entry)

XX B lymphocyte affinity maturation library peptide #107.

KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;

KW allergy; proliferative disease; infectious disease; arteriosclerosis;

KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;

KW ischaemia; graft-versus-host disease; neurodegenerative disease;

KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;

KW neuroprotective; cycostatic; immunostimulant; antitumour; anti-HIV;

KW antiaesthetic; antiallergic; chryomimetic; antinaemic; haemostatic;

KW dermatological; antidiabetic; antihypertensive; hepatotropic;

KW antidiabetic; antihypertensive; hepatotropic;

XX Unidentified.

XX WO200216411-A2.

XX 28-FEB-2002.

XX 17-AUG-2001; 2001WO-US025850.

XX 18-AUG-2000; 2000US-0226700P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Belzter JP, Potter DM, Fleming TL, Rosen CA;

XX WPI; 2002-499775/53.

XX The treatment of various diseases e.g. rheumatoid arthritis, comprises

XX administering B lymphocyte stimulator binding polypeptide.

XX Claim 70; Page 216; 387pp; English.

XX The present invention relates to the treatment, prevention or

XX amelioration of a disease or disorder associated with: aberrant B

XX lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells

XX of haematopoietic origin; or proliferative disease; and reducing,

XX inhibiting or stimulating immunoglobulin production, B cell proliferation

XX and graft rejection involving administration of BlyS binding polypeptide.

XX The BlyS binding polypeptides are used in the treatment, prevention or

XX amelioration of diseases such as immune system diseases, proliferative

XX diseases, infectious diseases, arteriosclerosis, inflammatory disorders,

XX hypergammaglobulinaemia, blood clotting disorders, ischaemia, and

XX neurodegenerative diseases. The present sequence is a B lymphocyte

XX stimulator protein binding peptide

XX Sequence 14 AA;

SQ

Query Match 100.0%; Score 64; DB 5; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00094;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLWL 10  
| | | | | | | | | |  
| | | | | | | | | |

Db 3 WYDPLTKLWL 12

## RESULT 37

ABJ00737

ID ABJ00737 standard; peptide; 14 AA.

AC ABJ00737;

DT 05-SEP-2002 (first entry)

XX B lymphocyte affinity maturation library peptide #11.

KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;

KW allergy; proliferative disease; infectious disease; arteriosclerosis;

KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;

KW ischaemia; graft-versus-host disease; neurodegenerative disease;

KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;

KW neuroprotective; cycostatic; immunostimulant; antitumour; anti-HIV;

KW antiaesthetic; antiallergic; chryomimetic; antinaemic; haemostatic;

KW dermatological; antidiabetic; antihypertensive; hepatotropic;

KW antidiabetic; antihypertensive; hepatotropic;

XX Unidentified.

XX WO200216411-A2.

XX 28-FEB-2002.

XX 17-AUG-2001; 2001WO-US025850.

XX 18-AUG-2000; 2000US-0226700P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Belzter JP, Potter DM, Fleming TL, Rosen CA;

XX WPI; 2002-499775/53.

XX The treatment of various diseases e.g. rheumatoid arthritis, comprises

XX administering B lymphocyte stimulator binding polypeptide.

XX Claim 70; Page 214; 387pp; English.

XX The present invention relates to the treatment, prevention or

XX amelioration of a disease or disorder associated with: aberrant B

XX lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells

XX of haematopoietic origin; or proliferative disease; and reducing,

XX inhibiting or stimulating immunoglobulin production, B cell proliferation

XX and graft rejection involving administration of BlyS binding polypeptide.

XX The BlyS binding polypeptides are used in the treatment, prevention or

XX amelioration of diseases such as immune system diseases, proliferative

XX diseases, infectious diseases, arteriosclerosis, inflammatory disorders,

XX hypergammaglobulinaemia, blood clotting disorders, ischaemia, and

XX neurodegenerative diseases. The present sequence is a B lymphocyte

XX stimulator protein binding peptide

XX Sequence 14 AA;

SQ

Query Match 100.0%; Score 64; DB 5; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00094;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLWL 10  
| | | | | | | | | |  
| | | | | | | | | |

Db 3 WYDPLTKLWL 12

RESULT 38

ABJ00740

ID ABJ00740 standard; peptide; 14 AA.

AC ABJ00740;

DT 05-SEP-2002 (first entry)



```
XX XX WO200216411-A2.
PN XX
XX XX 28-FEB-2002.
PD XX
XX XX 17-AUG-2001; 2001WO-US025850.
PF XX
XX XX 18-AUG-2000; 2000US-0226700P.
PR XX
XX XX (HUMA-) HUMAN GENOME SCI INC.
PA XX
XX XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;
PI XX
XX XX WPI; 2002-499775/53.
DR XX
XX XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide.
XX XX
XX XX Claim 70; Page 215; 387pp; English.
PS XX
XX XX The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of Blys binding polypeptide.
CC The Blys binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of haematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
CC
XX
SQ Sequence 14 AA;
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKLML 10
   |||||
   3 WYDPLTKLML 12
Db
RESULT 41
ABJ00802
ID ABJ00802 standard; peptide; 14 AA.
XX
XX AC ABJ00802;
XX
XX DT 05-SEP-2002 (first entry)
XX
XX DE B lymphocyte affinity maturation library peptide #76.
XX
XX KW B lymphocyte stimulator protein binding protein; Blys; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antineumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antiaesthetic; anti-allergic; thyromimetic; antinaemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; opthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
XX OS Unidentified.
XX
XX PN WO200216411-A2.
XX
XX PD 28-FEB-2002.
XX
XX PF 17-AUG-2001; 2001WO-US025850.
XX
XX PR 18-AUG-2000; 2001WO-US025850.
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PR 18-AUG-2000; 2000US-0226700P.
XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX
XX DR WPI; 2002-499775/53.
XX
XX PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
XX administering B lymphocyte stimulator binding polypeptide.
XX
XX PS Claim 70; Page 215; 387pp; English.
XX
XX CC The present invention relates to the treatment, prevention or
XX CC amelioration of a disease or disorder associated with: aberrant B
XX CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
XX CC of haematopoietic origin; or proliferative disease; and reducing,
XX CC inhibiting or stimulating immunoglobulin production, B cell proliferation
XX CC and graft rejection involving administration of Blys binding polypeptide.
XX CC The Blys binding polypeptides are used in the treatment, prevention or
XX CC amelioration of diseases such as immune system diseases, proliferative
XX CC diseases, diseases of cells of haematopoietic origin, graft rejection,
XX CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
XX CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
XX CC neurodegenerative diseases. The present sequence is a B lymphocyte
XX CC stimulator protein binding peptide
XX
XX
SQ Sequence 14 AA;
Query Match 100.0%; Score 64; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKLML 10
   |||||
   3 WYDPLTKLML 12
Db
RESULT 42
ABJ00815
ID ABJ00815 standard; peptide; 14 AA.
XX
XX AC ABJ00815;
XX
XX DT 05-SEP-2002 (first entry)
XX
XX DE B lymphocyte affinity maturation library peptide #89.
XX
XX KW B lymphocyte stimulator protein binding protein; Blys; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antineumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antiaesthetic; anti-allergic; thyromimetic; antinaemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; opthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
XX OS Unidentified.
XX
XX PN WO200216411-A2.
XX
XX PD 28-FEB-2002.
XX
XX PF 17-AUG-2001; 2001WO-US025850.
XX
XX PR 18-AUG-2000; 2000US-0226700P.
XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX
XX DR WPI; 2002-499775/53.
```

XX The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.  
XX  
XX Claim 70; Page 215; 387pp; English.  
PS  
XX The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of Blys binding polypeptide.  
CC The Blys binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of haematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
SQ Sequence 14 AA;  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 WYDPLTKLML 10  
DB 3 WYDPLTKLML 12  
RESULT 43  
ABJ00829  
ID ABJ00829 standard; peptide; 14 AA.  
XX  
XX ABJ00829;  
AC  
XX  
XX 05-SEP-2002 (first entry)  
DT  
XX  
XX B lymphocyte affinity maturation library peptide #103.  
DE  
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;  
XX allergy; proliferative disease; infectious disease; arteriosclerosis;  
XX inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
XX ischaemia; graft-versus-host disease; neurodegenerative disease;  
XX immunosuppressive; nephrotropic; antineumatic; antiarthritic;  
XX neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
XX antiasthmatic; antiallergic; thyromimetic; antianemic; haemostatic;  
XX dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
XX antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
XX Unidentified.  
OS  
XX  
XX WO200216411-A2.  
PN  
XX  
XX 28-FEB-2002.  
PD  
XX  
XX 17-AUG-2001; 2001WO-US025850.  
PF  
XX  
XX 18-AUG-2000; 2000US-0226700P.  
PR  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX  
XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
PI  
XX  
XX WPI; 2002-499775/53.  
DR  
XX  
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.  
XX  
XX Claim 70; Page 216; 387pp; English.  
PS  
XX  
XX The present invention relates to the treatment, prevention or

CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of Blys binding polypeptide.  
CC The Blys binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of haematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
SQ Sequence 14 AA;  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 WYDPLTKLML 10  
DB 3 WYDPLTKLML 12  
RESULT 44  
ABJ00729  
ID ABJ00729 standard; peptide; 14 AA.  
XX  
XX ABJ00729;  
AC  
XX  
XX 05-SEP-2002 (first entry)  
DT  
XX  
XX B lymphocyte affinity maturation library peptide #3.  
DE  
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;  
XX allergy; proliferative disease; infectious disease; arteriosclerosis;  
XX inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
XX ischaemia; graft-versus-host disease; neurodegenerative disease;  
XX immunosuppressive; nephrotropic; antineumatic; antiarthritic;  
XX neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
XX antiasthmatic; antiallergic; thyromimetic; antianemic; haemostatic;  
XX dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
XX antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
XX Unidentified.  
OS  
XX  
XX WO200216411-A2.  
PN  
XX  
XX 28-FEB-2002.  
PD  
XX  
XX 17-AUG-2001; 2001WO-US025850.  
PF  
XX  
XX 18-AUG-2000; 2000US-0226700P.  
PR  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX  
XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
PI  
XX  
XX WPI; 2002-499775/53.  
DR  
XX  
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.  
XX  
XX Claim 70; Page 214; 387pp; English.  
PS  
XX  
XX The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of Blys binding polypeptide.  
CC The Blys binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative

CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide

XX  
SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10  
|||||||  
3 WYDPLTKLML 12

DB

RESULT 45  
ABJ00756  
ID ABJ00756 standard; peptide; 14 AA.

XX

AC ABJ00756;

XX

DT 05-SEP-2002 (first entry)

XX

DE B lymphocyte affinity maturation library peptide #30.

KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neuroprotective; cytostatic; immunostimulant; antitumor; anti-HIV;  
KW antiaesthetic; antiallergic; chryomimetic; antianemic; haemostatic;  
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.

XX  
OS Undenified.

XX  
PN WO200216411-A2.

XX

PD 28-FEB-2002.

XX

XX 17-AUG-2001; 2001WO-US025850.

XX

PF 18-AUG-2000; 2000US-0226700P.

XX

PR (HUMA-) HUMAN GENOME SCI INC.

XX

PA Beltzer JP, Potter DM, Fleming TL, Rosen CA;

XX

PI WPI; 2002-499775/53.

XX

DR The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.

XX

PS Claim 70; Page 214; 387pp; English.

XX

CC The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of BlyS binding polypeptide.  
CC The BlyS binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide

XX  
SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10  
|||||||  
3 WYDPLTKLML 12

DB

RESULT 46  
ABJ00785  
ID ABJ00785 standard; peptide; 14 AA.

XX

AC ABJ00785;

XX

DT 05-SEP-2002 (first entry)

XX

DE B lymphocyte affinity maturation library peptide #59.

KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neuroprotective; cytostatic; immunostimulant; antitumor; anti-HIV;  
KW antiaesthetic; antiallergic; chryomimetic; antianemic; haemostatic;  
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.

XX  
OS Undenified.

XX  
PN WO200216411-A2.

XX

PD 28-FEB-2002.

XX

PF 17-AUG-2001; 2001WO-US025850.

XX

PR 18-AUG-2000; 2000US-0226700P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;

XX

PS WPI; 2002-499775/53.

XX

DR The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.

XX

PS Claim 70; Page 215; 387pp; English.

XX

CC The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of BlyS binding polypeptide.  
CC The BlyS binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide

XX  
SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10  
|||||||

DB 3 WYDPLTKLML 12

RESULT 47

ABJ00790 standard; peptide; 14 AA.

AC ABJ00790;

DT 05-SEP-2002 (first entry)

B lymphocyte affinity maturation library peptide #64.

B lymphocyte stimulator protein binding protein; BlyS; immune disease; allergy; proliferative disease; infectious disease; arteriosclerosis; inflammatory disorder; hypergammaglobulinaemia; blood clotting; ischaemia; graft-versus-host disease; neurodegenerative disease; immunosuppressive; nephrotropic; antirheumatic; antiarthritic; neuropsychiatric; cytosolic; immunostimulant; antitumour; anti-HIV; antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic; dermatological; antiinflammatory; cardiac; ophthalmological; uropathic; antidiabetic; antithyroid; antidepressant; hepatotropic.

OS Unidentified.

PN WO200216411-A2.

PD 28-FEB-2002.

PF 17-AUG-2001; 2001WO-US025850.

PR 18-AUG-2000; 2000US-0226700P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;

DR WPI; 2002-499775/53.

PT The treatment of various diseases e.g. rheumatoid arthritis, comprises administering B lymphocyte stimulator binding polypeptide.

PS Claim 70; Page 215; 387pp; English.

XX The present invention relates to the treatment, prevention or amelioration of a disease or disorder associated with: aberrant B lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells of haematopoietic origin; or proliferative disease; and reducing, inhibiting or stimulating immunoglobulin production, B cell proliferation and graft rejection involving administration of BlyS binding polypeptide. CC The BlyS binding polypeptides are used in the treatment, prevention or amelioration of diseases such as immune system diseases, proliferative diseases, diseases of cells of haematopoietic origin, graft rejection, allergies, infectious diseases, arteriosclerosis, inflammatory disorders, hypergammaglobulinaemia, blood clotting disorders, ischaemia, and neurodegenerative diseases. The present sequence is a B lymphocyte stimulator protein binding peptide

SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00094; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10

DB 3 WYDPLTKLML 12

RESULT 48

ABJ00792 standard; peptide; 14 AA.

XX

AC ABJ00792;

DT 05-SEP-2002 (first entry)

B lymphocyte affinity maturation library peptide #66.

B lymphocyte stimulator protein binding protein; BlyS; immune disease; allergy; proliferative disease; infectious disease; arteriosclerosis; inflammatory disorder; hypergammaglobulinaemia; blood clotting; ischaemia; graft-versus-host disease; neurodegenerative disease; immunosuppressive; nephrotropic; antirheumatic; antiarthritic; neuropsychiatric; cytosolic; immunostimulant; antitumour; anti-HIV; antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic; dermatological; antiinflammatory; cardiac; ophthalmological; uropathic; antidiabetic; antithyroid; antidepressant; hepatotropic.

OS Unidentified.

PN WO200216411-A2.

PD 28-FEB-2002.

PF 17-AUG-2001; 2001WO-US025850.

PR 18-AUG-2000; 2000US-0226700P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;

DR WPI; 2002-499775/53.

PT The treatment of various diseases e.g. rheumatoid arthritis, comprises administering B lymphocyte stimulator binding polypeptide.

PS Claim 70; Page 215; 387pp; English.

XX The present invention relates to the treatment, prevention or amelioration of a disease or disorder associated with: aberrant B lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells of haematopoietic origin; or proliferative disease; and reducing, inhibiting or stimulating immunoglobulin production, B cell proliferation and graft rejection involving administration of BlyS binding polypeptide. CC The BlyS binding polypeptides are used in the treatment, prevention or amelioration of diseases such as immune system diseases, proliferative diseases, diseases of cells of haematopoietic origin, graft rejection, allergies, infectious diseases, arteriosclerosis, inflammatory disorders, hypergammaglobulinaemia, blood clotting disorders, ischaemia, and neurodegenerative diseases. The present sequence is a B lymphocyte stimulator protein binding peptide

SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00094; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10

DB 3 WYDPLTKLML 12

RESULT 49

ABJ00732 standard; peptide; 14 AA.

AC ABJ00732;

DT 05-SEP-2002 (first entry)

B lymphocyte affinity maturation library peptide #6.

B lymphocyte stimulator protein binding protein; BlyS; immune disease;



KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
 KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;  
 KW antiaesthetic; antiallergic; thymometric; antianemic; haemostatic;  
 KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200216411-A2.  
 XX  
 PD 28-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-US025850.  
 XX  
 PR 18-AUG-2000; 2000US-0226700P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
 XX  
 PS Claim 70; Page 214; 387PP; English.  
 XX  
 CC The present invention relates to the treatment, prevention or  
 CC amelioration of a disease or disorder associated with: aberrant B  
 CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
 CC of haematopoietic origin; or proliferative disease; and reducing,  
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
 CC and graft rejection involving administration of Blys binding polypeptide.  
 CC The Blys binding polypeptides are used in the treatment, prevention or  
 CC amelioration of diseases such as immune system diseases, proliferative  
 CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
 CC neurodegenerative diseases. The present sequence is a B lymphocyte  
 CC stimulator protein binding peptide  
 CC  
 SO Sequence 14 AA;  
 Query Match 100.0%; Score 64; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.00094;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 WYDPLTKLWL 10  
 |||||  
 3 WYDPLTKLWL 12  
 DB  
 RESULT 50  
 ABJ00742 standard; peptide; 14 AA.  
 ID ABJ00742;  
 AC ABJ00742;  
 XX  
 DT 05-SEP-2002 (first entry)  
 XX  
 DE B lymphocyte affinity maturation library peptide #16.  
 XX  
 KW B lymphocyte stimulator protein binding protein; Blys; immune disease;  
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
 KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;  
 KW antiaesthetic; antiallergic; thymometric; antianemic; haemostatic;  
 KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;

KW antidiabetic; antithyroid; antidepressant; hepatropic.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200216411-A2.  
 XX  
 PD 28-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-US025850.  
 XX  
 PR 18-AUG-2000; 2000US-0226700P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
 XX  
 PS Claim 70; Page 214; 387PP; English.  
 XX  
 CC The present invention relates to the treatment, prevention or  
 CC amelioration of a disease or disorder associated with: aberrant B  
 CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
 CC of haematopoietic origin; or proliferative disease; and reducing,  
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
 CC and graft rejection involving administration of Blys binding polypeptide.  
 CC The Blys binding polypeptides are used in the treatment, prevention or  
 CC amelioration of diseases such as immune system diseases, proliferative  
 CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
 CC neurodegenerative diseases. The present sequence is a B lymphocyte  
 CC stimulator protein binding peptide  
 CC  
 SO Sequence 14 AA;  
 Query Match 100.0%; Score 64; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.00094;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 WYDPLTKLWL 10  
 |||||  
 3 WYDPLTKLWL 12  
 DB  
 RESULT 51  
 ABJ00757 standard; peptide; 14 AA.  
 ID ABJ00757;  
 AC ABJ00757;  
 XX  
 DT 05-SEP-2002 (first entry)  
 XX  
 DE B lymphocyte affinity maturation library peptide #31.  
 XX  
 KW B lymphocyte stimulator protein binding protein; Blys; immune disease;  
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
 KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;  
 KW antiaesthetic; antiallergic; thymometric; antianemic; haemostatic;  
 KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200216411-A2.  
 XX  
 PD 28-FEB-2002.

XX 17-AUG-2001; 2001WO-US025850.  
PF 18-AUG-2000; 2000US-0226700P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
XX WPI; 2002-499775/53.  
XX  
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.  
XX  
XX Claim 70; Page 214; 387pp; English.  
XX  
XX The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of Blys binding polypeptide.  
CC The Blys binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of haematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
XX Sequence 14 AA;  
SQ  
Query Match                    100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity    100.0%; Pred. No. 0.00094;  
Matches    10; Conservative    0; Mismatches    0; Indels    0; Gaps    0;  
OY            1 WYDPLTKLML 10  
             |||||  
             3 WYDPLTKLML 12  
DB  
RESULT 52  
ABJ00758                    100.0%; Score 64; DB 5; Length 14;  
ID ABJ00758 standard; peptide; 14 AA.  
XX  
XX ABJ00758;  
AC  
XX  
XX 05-SEP-2002 (first entry)  
DT  
XX  
XX B lymphocyte affinity maturation library peptide #32.  
DE  
XX  
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
KW antiaesthetic; antiallergic; thymometric; antianemic; haemostatic;  
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
XX Unidentified.  
OS  
XX  
XX WO200216411-A2.  
PN  
XX  
XX 28-FEB-2002.  
PD  
XX  
XX 17-AUG-2001; 2001WO-US025850.  
PF  
XX  
XX 18-AUG-2000; 2000US-0226700P.  
PR  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX

PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
XX WPI; 2002-499775/53.  
XX  
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.  
XX  
XX Claim 70; Page 214; 387pp; English.  
XX  
XX The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of Blys binding polypeptide.  
CC The Blys binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of haematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
XX Sequence 14 AA;  
SQ  
Query Match                    100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity    100.0%; Pred. No. 0.00094;  
Matches    10; Conservative    0; Mismatches    0; Indels    0; Gaps    0;  
OY            1 WYDPLTKLML 10  
             |||||  
             3 WYDPLTKLML 12  
DB  
RESULT 53  
ABJ00761                    100.0%; Score 64; DB 5; Length 14;  
ID ABJ00761 standard; peptide; 14 AA.  
XX  
XX ABJ00761;  
AC  
XX  
XX 05-SEP-2002 (first entry)  
DT  
XX  
XX B lymphocyte affinity maturation library peptide #35.  
DE  
XX  
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
KW antiaesthetic; antiallergic; thymometric; antianemic; haemostatic;  
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
XX Unidentified.  
OS  
XX  
XX WO200216411-A2.  
PN  
XX  
XX 28-FEB-2002.  
PD  
XX  
XX 17-AUG-2001; 2001WO-US025850.  
PF  
XX  
XX 18-AUG-2000; 2000US-0226700P.  
PR  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX  
XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
XX WPI; 2002-499775/53.  
XX  
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.  
XX

PS Claim 70; Page 214; 387pp; English.

XX The present invention relates to the treatment, prevention or

CC amelioration of a disease or disorder associated with: aberrant B

CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells

CC of haematopoietic origin; or proliferative disease; and reducing,

CC inhibiting or stimulating immunoglobulin production, B cell proliferation

CC and graft rejection involving administration of Blys binding polypeptide.

CC The Blys binding polypeptides are used in the treatment, prevention or

CC amelioration of diseases such as immune system diseases, proliferative

CC diseases, diseases of cells of hematopoietic origin, graft rejection,

CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,

CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and

CC neurodegenerative diseases. The present sequence is a B lymphocyte

CC stimulator protein binding peptide

SQ Sequence 14 AA;

QY Query Match 100.0%; Score 64; DB 5; Length 14;

DB Best Local Similarity 100.0%; Pred. No. 0.00094;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 WYDPLTKLML 10

3 WYDPLTKLML 12

RESULT 54

ABJ00769 standard; peptide; 14 AA.

ABJ00769;

05-SEP-2002 (first entry)

B lymphocyte affinity maturation library peptide #43.

B lymphocyte stimulator protein binding protein; Blys; immune disease;

allergy; proliferative disease; infectious disease; arteriosclerosis;

inflammatory disorder; hypergammaglobulinaemia; blood clotting;

ischaemia; graft-versus-host disease; neurodegenerative disease;

immunosuppressive; nephrotropic; antirheumatic; antiarthritic;

neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;

antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;

dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;

antidiabetic; antithyroid; antidepressant; hepatotropic.

Unidentified.

WO200216411-A2.

28-FEB-2002.

17-AUG-2001; 2001WO-US025850.

18-AUG-2000; 2000US-0226700P.

(HUMA-) HUMAN GENOME SCI INC.

Beltzer JP, Potter DM, Fleming TL, Rosen CA;

WPI; 2002-499775/53.

The treatment of various diseases e.g. rheumatoid arthritis, comprises

administering B lymphocyte stimulator binding polypeptide.

Claim 70; Page 214; 387pp; English.

The present invention relates to the treatment, prevention or

amelioration of a disease or disorder associated with: aberrant B

lymphocyte stimulator (Blys), Blys receptor expression or activity; cells

of haematopoietic origin; or proliferative disease; and reducing,

inhibiting or stimulating immunoglobulin production, B cell proliferation

and graft rejection involving administration of Blys binding polypeptide.

The Blys binding polypeptides are used in the treatment, prevention or

amelioration of diseases such as immune system diseases, proliferative

diseases, diseases of cells of hematopoietic origin, graft rejection,

allergies, infectious diseases, arteriosclerosis, inflammatory disorders,

hypergammaglobulinaemia, blood clotting disorders, ischaemia, and

neurodegenerative diseases. The present sequence is a B lymphocyte

stimulator protein binding peptide

CC and graft rejection involving administration of Blys binding polypeptide.

CC The Blys binding polypeptides are used in the treatment, prevention or

CC amelioration of diseases such as immune system diseases, proliferative

CC diseases, diseases of cells of hematopoietic origin, graft rejection,

CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,

CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and

CC neurodegenerative diseases. The present sequence is a B lymphocyte

CC stimulator protein binding peptide

SQ Sequence 14 AA;

QY Query Match 100.0%; Score 64; DB 5; Length 14;

DB Best Local Similarity 100.0%; Pred. No. 0.00094;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 WYDPLTKLML 10

3 WYDPLTKLML 12

RESULT 55

ABJ00780 standard; peptide; 14 AA.

ABJ00780;

05-SEP-2002 (first entry)

B lymphocyte affinity maturation library peptide #54.

B lymphocyte stimulator protein binding protein; Blys; immune disease;

allergy; proliferative disease; infectious disease; arteriosclerosis;

inflammatory disorder; hypergammaglobulinaemia; blood clotting;

ischaemia; graft-versus-host disease; neurodegenerative disease;

immunosuppressive; nephrotropic; antirheumatic; antiarthritic;

neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;

antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;

dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;

antidiabetic; antithyroid; antidepressant; hepatotropic.

Unidentified.

WO200216411-A2.

28-FEB-2002.

17-AUG-2001; 2001WO-US025850.

18-AUG-2000; 2000US-0226700P.

(HUMA-) HUMAN GENOME SCI INC.

Beltzer JP, Potter DM, Fleming TL, Rosen CA;

WPI; 2002-499775/53.

The treatment of various diseases e.g. rheumatoid arthritis, comprises

administering B lymphocyte stimulator binding polypeptide.

Claim 70; Page 215; 387pp; English.

The present invention relates to the treatment, prevention or

amelioration of a disease or disorder associated with: aberrant B

lymphocyte stimulator (Blys), Blys receptor expression or activity; cells

of haematopoietic origin; or proliferative disease; and reducing,

inhibiting or stimulating immunoglobulin production, B cell proliferation

and graft rejection involving administration of Blys binding polypeptide.

The Blys binding polypeptides are used in the treatment, prevention or

amelioration of diseases such as immune system diseases, proliferative

diseases, diseases of cells of hematopoietic origin, graft rejection,

allergies, infectious diseases, arteriosclerosis, inflammatory disorders,

hypergammaglobulinaemia, blood clotting disorders, ischaemia, and

neurodegenerative diseases. The present sequence is a B lymphocyte

CC stimulator protein binding peptide  
XX  
SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10  
DB 3 WYDPLTKLML 12

RESULT 56  
ABU00781  
ID ABU00781 standard; peptide; 14 AA.

AC ABU00781;  
XX  
XX 05-SEP-2002 (first entry)

DE B lymphocyte affinity maturation library peptide #55.

XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KW allergic; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neuroprotective; cytosolic; immunostimulant; antitumour; anti-HIV;  
KW antiaesthetic; antiallergic; thymometric; antianemic; haemostatic;  
KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.

XX Unidentified.

OS WO200216411-A2.

XX 28-FEB-2002.

PD 17-AUG-2001; 2001WO-US025850.

PF 18-AUG-2000; 2000US-0226700P.

PR (HUMA-) HUMAN GENOME SCI INC.

PA Beltzer JP, Potter DM, Fleming TL, Rosen CA;

PI WPI; 2002-499775/53.

DR The treatment of various diseases e.g. rheumatoid arthritis, comprises  
XX administering B lymphocyte stimulator binding polypeptide.

PS Claim 70; Page 215; 387pp; English.

XX The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of BlyS binding polypeptide.  
CC The BlyS binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide

SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10  
DB 3 WYDPLTKLML 12

RESULT 57  
ABU00789  
ID ABU00789 standard; peptide; 14 AA.

AC ABU00789;  
XX  
XX 05-SEP-2002 (first entry)

DE B lymphocyte affinity maturation library peptide #63.

XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KW allergic; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neuroprotective; cytosolic; immunostimulant; antitumour; anti-HIV;  
KW antiaesthetic; antiallergic; thymometric; antianemic; haemostatic;  
KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.

XX Unidentified.

OS WO200216411-A2.

XX 28-FEB-2002.

PD 17-AUG-2001; 2001WO-US025850.

PF 18-AUG-2000; 2000US-0226700P.

PR (HUMA-) HUMAN GENOME SCI INC.

PA Beltzer JP, Potter DM, Fleming TL, Rosen CA;

PI WPI; 2002-499775/53.

DR The treatment of various diseases e.g. rheumatoid arthritis, comprises  
XX administering B lymphocyte stimulator binding polypeptide.

PS Claim 70; Page 215; 387pp; English.

XX The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of BlyS binding polypeptide.  
CC The BlyS binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide

SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10  
DB 3 WYDPLTKLML 12

RESULT 58

ID	ABJ00806	standard; peptide; 14 AA.
AC	ABJ00806;	
DT	05-SEP-2002	(first entry)
XX	B lymphocyte affinity maturation library peptide #80.	
XX		
KW	B lymphocyte stimulator protein binding protein; BLyS; immune disease;	
KM	allergy; proliferative disease; infectious disease; arteriosclerosis;	
KM	inflammatory disorder; hypergammaglobulinaemia; blood clotting;	
KW	ischaemia; graft-versus-host disease; neurodegenerative disease;	
KM	immunoprotective; nephrotropic; antirheumatic; antiarthritis;	
KW	neuroprotective; cytostatic; immunostimulant; antitumor; anti-HIV;	
KM	antiaesthetic; antiallergic; thyromimetic; antinaemic; haemostatic;	
KW	dermatological; antiflammatory; cardiac; ophthalmologically; uropathic;	
KX	antidiabetic; antithyroid; antidepressant; hepatotropic.	
OS	Unidentified.	
XX		
PN	WO200216411-A2.	
XX		
PD	28-FEB-2002.	
XX		
PF	17-AUG-2001; 2001WO-US025850.	
XX		
PR	18-AUG-2000; 2000US-0226700P.	
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
PI	Beltzer JP, Potter DM, Fleming TL, Rosen CA;	
DR	WPI; 2002-499775/53.	
XX		
PT	The treatment of various diseases e.g. rheumatoid arthritis, comprises	
FT	administering B lymphocyte stimulator binding polypeptide.	
XX		
PS	Claim 70; Page 215; 387pp; English.	
XX		
CC	The present invention relates to the treatment, prevention or	
CC	amelioration of a disease or disorder associated with: aberrant B	
CC	lymphocyte stimulator (BLyS), BLyS receptor expression or activity; cells	
CC	of haematopoietic origin; or proliferative disease; and reducing,	
CC	inhibiting or stimulating immunoglobulin production, B cell proliferation	
CC	and graft rejection involving administration of BLyS binding polypeptide.	
CC	The BLyS binding polypeptides are used in the treatment, prevention or	
CC	amelioration of diseases such as immune system diseases, proliferative	
CC	diseases, diseases of cells of hematopoietic origin, graft rejection,	
CC	allergies, infectious diseases, arteriosclerosis, inflammatory disorders,	
CC	hypergammaglobulinaemia, blood clotting disorders, ischaemia, and	
CC	neurodegenerative diseases. The present sequence is a B lymphocyte	
CC	stimulator protein binding peptide	
SQ	Sequence 14 AA;	
OY	Query Match	100.0%; Score 64; DB 5; Length 14;
Dd	Best Local Similarity	100.0%; Pred. NO. 0.00094;
XX	Matches 10; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
XX	1 WYDPLTKLML 10	
XX		
XX	3 WYDPLTKLML 12	
XX		
XX	RESULT 59	
XX	ABJ00817	
XX	ABJ00817 standard; peptide; 14 AA.	
XX	ABJ00817;	
XX	05-SEP-2002 (first entry)	
XX		

DE	B lymphocyte affinity maturation library peptide #91.
XX	
XX	B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KM	allergy; proliferative disease; infectious disease; arteriosclerosis;
KM	inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KM	ischaemia; graft-versus-host disease; neurodegenerative disease;
KM	immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KM	neuroprotective; cytosolic; immunostimulant; antitumour; anti-HIV;
KM	antiaesthetic; anti-allergic; thyromimetic; antanaemic; haemostatic;
KM	dermatological; anti-inflammatory; cardiac; ophthalmological; uropathic;
XX	antidiabetic; antithyroid; antidepressant; hepatotropic.
OS	Unidentified.
XX	
PN	WO200216411-A2.
XX	
PD	28-FEB-2002.
XX	
PF	17-AUG-2001; 2001WO-US025650.
XX	
PR	18-AUG-2000; 2000US-0226700P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PJ	Belzter JP, Potter DM, Fleming TL, Rosen CA,
DR	WPI; 2002-499775/53.
XX	
PT	The treatment of various diseases e.g. rheumatoid arthritis, comprises
PS	administering B lymphocyte stimulator binding polypeptide.
XX	
PS	Claim 70; Page 215; 387pp; English.
XX	
CC	The present invention relates to the treatment, prevention or
CC	amelioration of a disease or disorder associated with: aberrant B
CC	lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
CC	of haematopoietic origin; or proliferative disease; and reducing,
CC	inhibiting or stimulating immunoglobulin production, B cell proliferation
CC	and graft rejection involving administration of BlyS binding polypeptide.
CC	The BlyS binding polypeptides are used in the treatment, prevention or
CC	amelioration of diseases such as immune system diseases, proliferative
CC	diseases, diseases of cells of hematopoietic origin, graft rejection,
CC	allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC	hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC	neurodegenerative diseases. The present sequence is a B lymphocyte
CC	stimulator protein binding peptide
XX	
SC	Sequence 14 AA;
Query Match	100.0%; Score 64; DB 5; Length 14;
Best Local Similarity	100.0%; Pred. No. 0.00094;
Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 WYDPLTKLWL 10       
DB	3 WYDPLTKLWL 12
RESULT 60	
ABU00752	
ID	ABU00752 standard; peptide; 14 AA.
XX	
AC	ABU00752;
XX	
DT	05-SEP-2002 (first entry)
XX	
DE	B lymphocyte affinity maturation library peptide #26.
XX	
KM	B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KM	allergy; proliferative disease; infectious disease; arteriosclerosis;
KM	inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KM	ischaemia; graft-versus-host disease; neurodegenerative disease;
KM	immunosuppressive; nephrotropic; antineuritic; antiarthritic;

KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;  
 KW antiasthmatic; antiallergic; thyromimetic; antianemic; haemostatic;  
 KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
 XX unidentified.  
 OS  
 PN WO200216411-A2.  
 XX  
 XX 28-FEB-2002.  
 PD  
 XX 17-AUG-2001; 2001WO-US025850.  
 XX  
 XX 18-AUG-2000; 2000US-0226700P.  
 PR  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
 XX  
 XX WPI; 2002-499775/53.  
 DR  
 XX  
 PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
 XX administering B lymphocyte stimulator binding polypeptide.  
 XX  
 XX Claim 70; Page 214; 387pp; English.  
 PS  
 CC The present invention relates to the treatment, prevention or  
 CC amelioration of a disease or disorder associated with: aberrant B  
 CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
 CC of haematopoietic origin; or proliferative disease; and reducing,  
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
 CC and graft rejection involving administration of Blys binding polypeptide.  
 CC The Blys binding polypeptides are used in the treatment, prevention or  
 CC amelioration of diseases such as immune system diseases, proliferative  
 CC diseases, diseases of cells of haematopoietic origin, graft rejection,  
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
 CC neurodegenerative diseases. The present sequence is a B lymphocyte  
 CC stimulator protein binding peptide  
 CC  
 SQ Sequence 14 AA;  
 QY  
 Query Match 100.0%; Score 64; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.00094;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 WYDPLTKLML 10  
 3 WYDPLTKLML 12  
 RESULT 61  
 ID ABJ00811 standard; peptide; 14 AA.  
 AC ABJ00811;  
 XX  
 XX 05-SEP-2002 (first entry)  
 DT  
 XX  
 XX B lymphocyte affinity maturation library peptide #85.  
 DE  
 KW B lymphocyte stimulator protein binding protein; Blys; immune disease;  
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
 KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;  
 KW antiasthmatic; antiallergic; thyromimetic; antianemic; haemostatic;  
 KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
 XX  
 XX Unidentified.  
 OS  
 XX

PN WO200216411-A2.  
 XX  
 XX 28-FEB-2002.  
 PD  
 XX 17-AUG-2001; 2001WO-US025850.  
 PF  
 XX 18-AUG-2000; 2000US-0226700P.  
 PR  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
 XX  
 XX WPI; 2002-499775/53.  
 DR  
 XX  
 PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
 XX administering B lymphocyte stimulator binding polypeptide.  
 XX  
 XX Claim 70; Page 215; 387pp; English.  
 PS  
 CC The present invention relates to the treatment, prevention or  
 CC amelioration of a disease or disorder associated with: aberrant B  
 CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
 CC of haematopoietic origin; or proliferative disease; and reducing,  
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
 CC and graft rejection involving administration of Blys binding polypeptide.  
 CC The Blys binding polypeptides are used in the treatment, prevention or  
 CC amelioration of diseases such as immune system diseases, proliferative  
 CC diseases, diseases of cells of haematopoietic origin, graft rejection,  
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
 CC neurodegenerative diseases. The present sequence is a B lymphocyte  
 CC stimulator protein binding peptide  
 CC  
 SQ Sequence 14 AA;  
 QY  
 Query Match 100.0%; Score 64; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.00094;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 WYDPLTKLML 10  
 3 WYDPLTKLML 12  
 RESULT 62  
 ID ABJ00812 standard; peptide; 14 AA.  
 AC ABJ00812;  
 XX  
 XX 05-SEP-2002 (first entry)  
 DT  
 XX  
 XX B lymphocyte affinity maturation library peptide #86.  
 DE  
 KW B lymphocyte stimulator protein binding protein; Blys; immune disease;  
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
 KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;  
 KW antiasthmatic; antiallergic; thyromimetic; antianemic; haemostatic;  
 KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
 XX  
 XX Unidentified.  
 OS  
 PN WO200216411-A2.  
 XX  
 XX 28-FEB-2002.  
 PD  
 XX 17-AUG-2001; 2001WO-US025850.  
 PF  
 XX 18-AUG-2000; 2000US-0226700P.  
 PR

XX (HUMA-) HUMAN GENOME SCI INC.  
XX PA  
XX PI Belzter JP, Potter DM, Fleming TL, Rosen CA;  
XX DR WPI; 2002-499775/53.  
XX PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
XX PT administering B lymphocyte stimulator binding polypeptide.  
XX PS  
XX PS Claim 70; Page 215; 387pp; English.  
XX CC The present invention relates to the treatment, prevention or  
XX CC amelioration of a disease or disorder associated with: aberrant B  
XX CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
XX CC of haematopoietic origin; or proliferative disease; and reducing,  
XX CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
XX CC and graft rejection involving administration of Blys binding polypeptide.  
XX CC The Blys binding polypeptides are used in the treatment, prevention or  
XX CC amelioration of diseases such as immune system diseases, proliferative  
XX CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
XX CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
XX CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
XX CC neurodegenerative diseases. The present sequence is a B lymphocyte  
XX CC stimulator protein binding peptide  
SQ Sequence 14 AA;  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WYDPLTKLML 10  
Db 3 WYDPLTKLML 12  
RESULT 63  
ABU00735  
ID ABU00735 standard; peptide; 14 AA.  
AC ABU00735;  
XX  
XX 05-SEP-2002 (first entry)  
DE  
XX B lymphocyte affinity maturation library peptide #9.  
DE  
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neuroprotective; cycostatic; immunostimulant; antitumour; anti-HIV;  
KW antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;  
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
XX Unidentified.  
OS  
XX WO200216411-A2.  
XX  
XX 28-FEB-2002.  
PD  
XX 17-AUG-2001; 2001WO-US025850.  
XX  
XX 18-AUG-2000; 2000US-0226700P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX PA  
XX Belzter JP, Potter DM, Fleming TL, Rosen CA;  
XX PI  
XX DR WPI; 2002-499775/53.  
XX

PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.  
PS  
PS Claim 70; Page 214; 387pp; English.  
XX  
XX The present invention relates to the treatment, prevention or  
XX CC amelioration of a disease or disorder associated with: aberrant B  
XX CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
XX CC of haematopoietic origin; or proliferative disease; and reducing,  
XX CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
XX CC and graft rejection involving administration of Blys binding polypeptide.  
XX CC The Blys binding polypeptides are used in the treatment, prevention or  
XX CC amelioration of diseases such as immune system diseases, proliferative  
XX CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
XX CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
XX CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
XX CC neurodegenerative diseases. The present sequence is a B lymphocyte  
XX CC stimulator protein binding peptide  
SQ Sequence 14 AA;  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WYDPLTKLML 10  
Db 3 WYDPLTKLML 12  
RESULT 64  
ABU00736  
ID ABU00736 standard; peptide; 14 AA.  
AC ABU00736;  
XX  
XX 05-SEP-2002 (first entry)  
DE  
XX B lymphocyte affinity maturation library peptide #10.  
DE  
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neuroprotective; cycostatic; immunostimulant; antitumour; anti-HIV;  
KW antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;  
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
XX Unidentified.  
OS  
XX WO200216411-A2.  
XX  
XX 28-FEB-2002.  
PD  
XX 17-AUG-2001; 2001WO-US025850.  
XX  
XX 18-AUG-2000; 2000US-0226700P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX PA  
XX Belzter JP, Potter DM, Fleming TL, Rosen CA;  
XX PI  
XX DR WPI; 2002-499775/53.  
XX  
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises  
XX PT administering B lymphocyte stimulator binding polypeptide.  
XX PS  
XX PS Claim 70; Page 214; 387pp; English.  
XX  
XX The present invention relates to the treatment, prevention or  
XX CC amelioration of a disease or disorder associated with: aberrant B

CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
CC of hematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of Blys binding polypeptide.  
CC The Blys binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinemia, blood clotting disorders, ischemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
CC  
SQ Sequence 14 AA;  
QY 1 WYDPLTKLWL 10  
Db 3 WYDPLTKLWL 12  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
RESULT 65  
ID ABJ00749 standard; peptide; 14 AA.  
XX  
AC ABJ00749;  
DT 05-SEP-2002 (first entry)  
DE B lymphocyte affinity maturation library peptide #23.  
XX  
DE B lymphocyte stimulator protein binding protein; Blys; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antineumatic; antiarthritic;  
KW neuroprotective; cytostatic; immunostimulant; antitumor; anti-HIV;  
KW antiaesthetic; antiallergic; thymometric; antianemic; haemostatic;  
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
OS Unidentified.  
XX WO200216411-A2.  
PN 28-FEB-2002.  
XX  
PD 17-AUG-2001; 2001WO-US025850.  
XX  
PF 18-AUG-2000; 2000US-0226700P.  
XX  
PR (HUMA-) HUMAN GENOME SCI INC.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Belzer JP, Potter DM, Fleming TL, Rosen CA;  
XX  
XX WPI; 2002-499775/53.  
DR The treatment of various diseases e.g. rheumatoid arthritis, comprises  
XX administering B lymphocyte stimulator binding polypeptide.  
XX  
PT Claim 70; Page 214; 387pp; English.  
XX  
XX The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
CC of hematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of Blys binding polypeptide.  
CC The Blys binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,

CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinemia, blood clotting disorders, ischemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
CC  
SQ Sequence 14 AA;  
QY 1 WYDPLTKLWL 10  
Db 3 WYDPLTKLWL 12  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
RESULT 66  
ID ABJ00762 standard; peptide; 14 AA.  
XX  
AC ABJ00762;  
DT 05-SEP-2002 (first entry)  
DE B lymphocyte affinity maturation library peptide #36.  
XX  
DE B lymphocyte stimulator protein binding protein; Blys; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antineumatic; antiarthritic;  
KW neuroprotective; cytostatic; immunostimulant; antitumor; anti-HIV;  
KW antiaesthetic; antiallergic; thymometric; antianemic; haemostatic;  
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
OS Unidentified.  
XX WO200216411-A2.  
PN 28-FEB-2002.  
XX  
PD 17-AUG-2001; 2001WO-US025850.  
XX  
PF 18-AUG-2000; 2000US-0226700P.  
XX  
PR (HUMA-) HUMAN GENOME SCI INC.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Belzer JP, Potter DM, Fleming TL, Rosen CA;  
XX  
XX WPI; 2002-499775/53.  
DR The treatment of various diseases e.g. rheumatoid arthritis, comprises  
XX administering B lymphocyte stimulator binding polypeptide.  
XX  
PT Claim 70; Page 214; 387pp; English.  
XX  
XX The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
CC of hematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of Blys binding polypeptide.  
CC The Blys binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinemia, blood clotting disorders, ischemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
CC  
SQ Sequence 14 AA;



Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10  
|||  
DB 3 WYDPLTKLML 12

## RESULT 67

ABJ00766 standard; peptide; 14 AA.

AC ABJ00766;

DT 05-SEP-2002 (first entry)

DE B lymphocyte affinity maturation library peptide #40.

KM B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KM allergy; proliferative disease; infectious disease; arteriosclerosis;  
KM inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KM ischaemia; graft-versus-host disease; neurodegenerative disease;  
KM immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KM neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
KM antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;  
KM dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KM antidiabetic; antithyroid; antidepressant; hepatotropic.

OS Unidentified.

PN WO200216411-A2.

PD 28-FEB-2002.

PF 17-AUG-2001; 2001WO-US025850.

PR 18-AUG-2000; 2000US-0226700P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;

DR WPI, 2002-499775/53.

PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
administering B lymphocyte stimulator binding polypeptide.

PS Claim 70; Page 214; 387pp; English.

XX The present invention relates to the treatment, prevention or  
XX amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of BlyS binding polypeptide.  
CC The BlyS binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of haematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide

XX Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10  
|||  
DB 3 WYDPLTKLML 12

## RESULT 68

ABJ00775 standard; peptide; 14 AA.

AC ABJ00775;

DT 05-SEP-2002 (first entry)

DE B lymphocyte affinity maturation library peptide #49.

KM B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KM allergy; proliferative disease; infectious disease; arteriosclerosis;  
KM inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KM ischaemia; graft-versus-host disease; neurodegenerative disease;  
KM immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KM neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
KM antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;  
KM dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KM antidiabetic; antithyroid; antidepressant; hepatotropic.

OS Unidentified.

PN WO200216411-A2.

PD 28-FEB-2002.

PF 17-AUG-2001; 2001WO-US025850.

PR 18-AUG-2000; 2000US-0226700P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;

DR WPI, 2002-499775/53.

PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
administering B lymphocyte stimulator binding polypeptide.

PS Claim 70; Page 215; 387pp; English.

XX The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of BlyS binding polypeptide.  
CC The BlyS binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of haematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide

XX Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10  
|||  
DB 3 WYDPLTKLML 12

## RESULT 69

ABJ00776 standard; peptide; 14 AA.

AC ABJ00776;

[illegible]

KW		inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KM		ischæmia, graft-versus-host disease; neurodegenerative diseases;
KX		immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KV		neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW		antiallergic; antiallergic; thyromimetic; antianaemic; haemostatic;
KM		dematological; antineoplastic; cardiac; ophthalmological; uropathic;
KX		antidiabetic; antithyroid; antidepressant; hepatotropic.
OS		Unidentified.
XX		
XX		WO200216411-A2.
PN		
PD		28-FEB-2002.
XX		
PP		17-AUG-2001; 2001WO-US025850.
XX		
PR		18-AUG-2000; 2000US-0226700P.
XX		
PA		(HUMA-) HUMAN GENOME SCI INC.
PI		Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX		
DR		WPI; 2002-499775/53.
XX		
PT		The treatment of various diseases e.g. rheumatoid arthritis, comprises
PS		administering B lymphocyte stimulator binding polypeptide.
CC		
PS		Claim 70; Page 216; 387pp; English.
XX		
CC		The present invention relates to the treatment, prevention or
CC		amelioration of a disease or disorder associated with: aberrant B
CC		lymphocyte stimulator (BLyS), BLyS receptor expression or activity; cells
CC		of haematopoietic origin; or proliferative disease; and reducing,
CC		inhibiting or stimulating immunoglobulin production, B cell proliferation
CC		and graft rejection involving administration of BLyS binding polypeptide.
CC		The BLyS binding polypeptides are used in the treatment, prevention or
CC		amelioration of diseases such as immune system diseases, proliferative
CC		diseases, diseases of cells of hematopoietic origin, graft rejection,
CC		allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC		hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC		neurodegenerative diseases. The present sequence is a B lymphocyte
CC		stimulator protein binding peptide
XX		
SQ		Sequence 14 AA:
	Query Match	100.0%; Score 64; DB 5; Length 14;
	Best Local Similarity	100.0%; Pred. No. 0.00094;
	Matches 10; Conservative	0; Mismatches 0; Indels 0; Gaps 0.
OY		1 WYDPPLTKLML 10
DB		3 WYDPPLTKLML 12
RESULT 71		
ID	ABJ00834	standard; peptide; 14 AA.
AC	ABU00834;	
XX		
DT	05-SEP-2002	(first entry)
DE		
B		lymphocyte affinity maturation library peptide #108.
B		lymphocyte stimulator protein binding protei; BLyS; immune disease;
KW		allergy; proliferative disease; infectious disease; arteriosclerosis;
KM		inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW		ischæmia; graft-versus-host disease; neurodegenerative disease;
KX		immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KV		neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW		antiallergic; antiallergic; thyromimetic; antianaemic; haemostatic;
KM		dermatological; antineoplastic; cardiac; ophthalmological; uropathic;
KX		antidiabetic; antithyroid; antidepressant; hepatotropic.

XX OS Unidentified.  
XX XX WO200216411-A2.  
XX PD 28-FEB-2002.  
XX PF 17-AUG-2001; 2001WO-US025850.  
XX PR 18-AUG-2000; 2000US-0226700P.  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
XX DR WPI; 2002-499775/53.  
XX PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
XX PT administering B lymphocyte stimulator binding polypeptide.  
XX PS Claim 70; Page 216; 387pp; English.  
XX CC The present invention relates to the treatment, prevention or  
XX CC amelioration of a disease or disorder associated with: aberrant B  
XX CC lymphocyte stimulator (BLyS), BLyS receptor expression or activity; cells  
XX CC of haematopoietic origin; or proliferative disease; and reducing,  
XX CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
XX CC and graft rejection involving administration of BLyS binding polypeptide.  
XX CC The BLyS binding polypeptides are used in the treatment, prevention or  
XX CC amelioration of diseases such as immune system diseases, proliferative  
XX CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
XX CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
XX CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
XX CC neurodegenerative diseases. The present sequence is a B lymphocyte  
XX CC stimulator protein binding peptide  
XX SQ Sequence 14 AA;  
XX  
XX Query Match 100.0%; Score 64; DB 5; Length 14;  
XX Best Local Similarity 100.0%; Pred. No. 0.00094;  
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 WYDPLTKLML 10  
XX |||||  
DB 3 WYDPLTKLML 12  
XX  
XX RESULT 72  
XX ID ABJ00728 standard; peptide; 14 AA.  
XX AC ABJ00728;  
XX XX  
XX DT 05-SEP-2002 (first entry)  
XX XX  
XX DE B lymphocyte affinity maturation library peptide #2.  
XX XX  
XX KW B lymphocyte stimulator protein binding protein; BLyS; immune disease;  
XX KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
XX KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
XX KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
XX KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
XX KW neuroprotective; cytosstatic; immunostimulant; antitumour; anti-HIV;  
XX KW antiaesthetic; antiallergic; thyromimetic; antianaemic; haemostatic;  
XX KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
XX KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX OS Unidentified.  
XX XX  
XX XX WO200216411-A2.  
XX XX  
XX XX 28-FEB-2002.  
XX PD

PF 17-AUG-2001; 2001WO-US025850.  
XX XX  
XX PR 18-AUG-2000; 2000US-0226700P.  
XX XX  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX XX  
XX PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
XX XX  
XX DR WPI; 2002-499775/53.  
XX XX  
XX PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
XX PT administering B lymphocyte stimulator binding polypeptide.  
XX PS Claim 70; Page 214; 387pp; English.  
XX XX  
XX CC The present invention relates to the treatment, prevention or  
XX CC amelioration of a disease or disorder associated with: aberrant B  
XX CC lymphocyte stimulator (BLyS), BLyS receptor expression or activity; cells  
XX CC of haematopoietic origin; or proliferative disease; and reducing,  
XX CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
XX CC and graft rejection involving administration of BLyS binding polypeptide.  
XX CC The BLyS binding polypeptides are used in the treatment, prevention or  
XX CC amelioration of diseases such as immune system diseases, proliferative  
XX CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
XX CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
XX CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
XX CC neurodegenerative diseases. The present sequence is a B lymphocyte  
XX CC stimulator protein binding peptide  
XX SQ Sequence 14 AA;  
XX  
XX Query Match 100.0%; Score 64; DB 5; Length 14;  
XX Best Local Similarity 100.0%; Pred. No. 0.00094;  
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 WYDPLTKLML 10  
XX |||||  
DB 3 WYDPLTKLML 12  
XX  
XX RESULT 73  
XX ID ABJ00747 standard; peptide; 14 AA.  
XX AC ABJ00747;  
XX XX  
XX DT 05-SEP-2002 (first entry)  
XX XX  
XX DE B lymphocyte affinity maturation library peptide #21.  
XX XX  
XX KW B lymphocyte stimulator protein binding protein; BLyS; immune disease;  
XX KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
XX KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
XX KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
XX KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
XX KW neuroprotective; cytosstatic; immunostimulant; antitumour; anti-HIV;  
XX KW antiaesthetic; antiallergic; thyromimetic; antianaemic; haemostatic;  
XX KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
XX KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX OS Unidentified.  
XX XX  
XX XX WO200216411-A2.  
XX XX  
XX XX 28-FEB-2002.  
XX PD  
XX PF 17-AUG-2001; 2001WO-US025850.  
XX XX  
XX PR 18-AUG-2000; 2000US-0226700P.  
XX XX  
XX XX (HUMA-) HUMAN GENOME SCI INC.  
XX XX  
XX XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;



CC The Blys binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
SQ Sequence 14 AA;  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WYDPLTKLWL 10  
Db 3 WYDPLTKLWL 12  
RESULT 76  
ABJ00763 standard; peptide; 14 AA.  
XX  
AC ABJ00763;  
XX  
DT 05-SEP-2002 (first entry)  
DE B lymphocyte affinity maturation library peptide #37.  
XX  
KW B lymphocyte stimulator protein binding protein; Blys; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neutrotective; cyostatic; immunostimulant; antitumour; anti-HIV;  
KW antiasclastic; anti-allergic; thymometric; antianemic; haemostatic;  
KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
OS Unidentified.  
XX  
PN WO200216411-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 17-AUG-2001; 2001WO-US025850.  
XX  
PR 18-AUG-2000; 2000US-0226700P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
P1 Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
XX  
XX WPI; 2002-499775/53.  
XX  
PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.  
XX  
PS Claim 70; Page 214; 387pp; English.  
XX  
CC The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with aberrant B  
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of Blys binding polypeptide.  
CC The Blys binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide

XX  
SQ Sequence 14 AA;  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WYDPLTKLWL 10  
Db 3 WYDPLTKLWL 12  
RESULT 77  
ABJ00779 standard; peptide; 14 AA.  
XX  
AC ABJ00779;  
XX  
DT 05-SEP-2002 (first entry)  
DE B lymphocyte affinity maturation library peptide #53.  
XX  
KW B lymphocyte stimulator protein binding protein; Blys; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neutrotective; cyostatic; immunostimulant; antitumour; anti-HIV;  
KW antiasclastic; anti-allergic; thymometric; antianemic; haemostatic;  
KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
OS Unidentified.  
XX  
PN WO200216411-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 17-AUG-2001; 2001WO-US025850.  
XX  
PR 18-AUG-2000; 2000US-0226700P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
P1 Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
XX  
XX WPI; 2002-499775/53.  
XX  
PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.  
XX  
PS Claim 70; Page 215; 387pp; English.  
XX  
CC The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with aberrant B  
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of Blys binding polypeptide.  
CC The Blys binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
SQ Sequence 14 AA;  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10  
| | | | |  
DB 3 WYDPLTKLML 12

## RESULT 78

ID ABJ00825 standard; peptide; 14 AA.

XX ABJ00825;

AC 05-SEP-2002 (first entry)

XX B lymphocyte affinity maturation library peptide #99.

XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
XX allergy; proliferative disease; infectious disease; arteriosclerosis;  
XX inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
XX ischaemia; graft-versus-host disease; neurodegenerative disease;  
XX immunosuppressive; nephrotropic; antineumatic; antiarthritic;  
XX immunoprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
XX antisthmatic; antiallergic; thyromimetic; antianaemic; haemostatic;  
XX dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
XX antidiabetic; antithyroid; antidepressant; hepatotropic.

OS Unidentified.

XX WO200216411-A2.

XX 28-FEB-2002.

XX 17-AUG-2001; 2001WO-US025850.

XX 18-AUG-2000; 2000US-0226700P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;

XX WPI; 2002-499775/53.

XX The treatment of various diseases e.g. rheumatoid arthritis, comprises  
XX administering B lymphocyte stimulator binding polypeptide.

XX Claim 70; Page 216; 387pp; English.

XX The present invention relates to the treatment, prevention or  
XX amelioration of a disease or disorder associated with: aberrant B  
XX lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells  
XX of haematopoietic origin; or proliferative disease; and reducing,  
XX inhibiting or stimulating immunoglobulin production, B cell proliferation  
XX and graft rejection involving administration of BlyS binding polypeptide.  
XX The BlyS binding polypeptides are used in the treatment, prevention or  
XX amelioration of diseases such as immune system diseases, proliferative  
XX diseases, diseases of cells of hematopoietic origin, graft rejection,  
XX allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
XX hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
XX neurodegenerative diseases. The present sequence is a B lymphocyte  
XX stimulator protein binding peptide

XX Sequence 14 AA;

XX Query Match 100.0%; Score 64; DB 5; Length 14;

XX Best Local Similarity 100.0%; Pred. No. 0.00094;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10  
| | | | |  
DB 3 WYDPLTKLML 12

RESULT 79  
ABJ00741

ID ABJ00741 standard; peptide; 14 AA.

XX ABJ00741;

AC 05-SEP-2002 (first entry)

XX B lymphocyte affinity maturation library peptide #15.

XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
XX allergy; proliferative disease; infectious disease; arteriosclerosis;  
XX inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
XX ischaemia; graft-versus-host disease; neurodegenerative disease;  
XX immunosuppressive; nephrotropic; antineumatic; antiarthritic;  
XX immunoprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
XX antisthmatic; antiallergic; thyromimetic; antianaemic; haemostatic;  
XX dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
XX antidiabetic; antithyroid; antidepressant; hepatotropic.

OS Unidentified.

XX WO200216411-A2.

XX 28-FEB-2002.

XX 17-AUG-2001; 2001WO-US025850.

XX 18-AUG-2000; 2000US-0226700P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;

XX WPI; 2002-499775/53.

XX The treatment of various diseases e.g. rheumatoid arthritis, comprises  
XX administering B lymphocyte stimulator binding polypeptide.

XX Claim 70; Page 214; 387pp; English.

XX The present invention relates to the treatment, prevention or  
XX amelioration of a disease or disorder associated with: aberrant B  
XX lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells  
XX of haematopoietic origin; or proliferative disease; and reducing,  
XX inhibiting or stimulating immunoglobulin production, B cell proliferation  
XX and graft rejection involving administration of BlyS binding polypeptide.  
XX The BlyS binding polypeptides are used in the treatment, prevention or  
XX amelioration of diseases such as immune system diseases, proliferative  
XX diseases, diseases of cells of hematopoietic origin, graft rejection,  
XX allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
XX hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
XX neurodegenerative diseases. The present sequence is a B lymphocyte  
XX stimulator protein binding peptide

XX Sequence 14 AA;

XX Query Match 100.0%; Score 64; DB 5; Length 14;

XX Best Local Similarity 100.0%; Pred. No. 0.00094;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10  
| | | | |  
DB 3 WYDPLTKLML 12

## RESULT 80

ID ABJ00772 standard; peptide; 14 AA.

XX ABJ00772;

AC 05-SEP-2002 (first entry)

XX B lymphocyte affinity maturation library peptide #46.

XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
 XX allergy; proliferative disease; infectious disease; arteriosclerosis;  
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
 KW immunosuppressive; nephrotropic; antihemetic; antiarthritic;  
 KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;  
 KW antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;  
 KW dermatological; antiinflammatory; cardial; ophthalmological; uropathic;  
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200216411-A2.  
 XX  
 PD 28-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-US025850.  
 XX  
 PR 18-AUG-2000; 2000US-0226700P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
 XX  
 DR WPI; 2002-499775/53.  
 XX  
 PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
 XX administering B lymphocyte stimulator binding polypeptide.  
 XX  
 PS Claim 70; Page 215; 387pp; English.  
 XX  
 CC The present invention relates to the treatment, prevention or  
 CC amelioration of a disease or disorder associated with: aberrant B  
 CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells  
 CC of haematopoietic origin; or proliferative disease; and reducing,  
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
 CC and graft rejection involving administration of BlyS binding polypeptide.  
 CC The BlyS binding polypeptides are used in the treatment, prevention or  
 CC amelioration of diseases such as immune system diseases, proliferative  
 CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
 CC neurodegenerative diseases. The present sequence is a B lymphocyte  
 CC stimulator protein binding peptide  
 XX  
 SO Sequence 14 AA;  
 XX  
 OY  
 DB 1 WYDPLTKLWL 10  
 3 WYDPLTKLWL 12  
 XX  
 RESULT 81  
 ID ABJ00774 standard; peptide; 14 AA.  
 AC ABJ00774;  
 XX  
 DT 05-SEP-2002 (first entry)  
 XX  
 DB B lymphocyte affinity maturation library peptide #48.  
 XX  
 KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
 KW immunosuppressive; nephrotropic; antihemetic; antiarthritic;  
 KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;  
 KW antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;  
 KW dermatological; antiinflammatory; cardial; ophthalmological; uropathic;  
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.

XX	OS	Unidentified.	antiaesthetic; anti-allergic; thyromimetic; antianemic; haemostatic; dermatological; anti-inflammatory; cardiant; ophthalmological; uropathic; antidiabetic; antithyroid; antidepressant; hepatotropic.
XX	XX		
XX	XX	WO200216411-A2.	
XX	XX		
XX	XX	28-FEB-2002.	
XX	XX		
XX	XX	17-AUG-2001; 2001WO-US025850.	
XX	XX		
XX	XX	18-AUG-2000; 2000US-0226700P.	
XX	XX		
XX	XX	(HUMA-) HUMAN GENOME SCI INC.	
XX	XX		
XX	XX	Beltzer JP, Potter DM, Fleming TL, Rosen CA;	
XX	XX	WPI; 2002-499775/53.	
XX	XX		
XX	XX		
XX	XX	Claim 70; Page 215; 387pp; English.	
XX	XX		
XX	XX	The present invention relates to the treatment, prevention or	
XX	XX	amelioration of a disease or disorder associated with: aberrant B	
XX	XX	lymphocyte stimulator (BLyS), BLyS receptor expression or activity; cells	
XX	XX	of haematopoietic origin; or proliferative disease; and reducing,	
XX	XX	inhibiting or stimulating immunoglobulin production, B cell proliferation	
XX	XX	and graft rejection involving administration of BLyS binding polypeptide.	
XX	XX	The BLyS binding polypeptides are used in the treatment, prevention or	
XX	XX	amelioration of diseases such as immune system diseases, proliferative	
XX	XX	diseases, diseases of cells of haematopoietic origin, graft rejection,	
XX	XX	allergies, infectious diseases, arteriosclerosis, inflammatory disorders,	
XX	XX	hyperimmunoglobulinaemia, blood clotting disorders, ischaemia, and	
XX	XX	neurodegenerative diseases. The present sequence is a B lymphocyte	
XX	XX	stimulator protein binding polypeptide	
XX	XX		
XX	XX	Sequence 14 AA;	
XX	XX		
XX	XX	Query Match	100.0%; Score 64; DB 5; Length 14;
XX	XX	Best Local Similarity	100.0%; Pred. No. 0.00094;
XX	XX	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX	XX		
XX	XX	1 WYDPLTKLML 10	
XX	XX		
XX	XX	3 WYDPLTKLML 12	
XX	XX		
XX	XX	RESULT 82	
XX	XX	ABJ00782	
XX	XX	ID	ABJ00782 standard; peptide; 14 AA.
XX	XX	ABJ00782;	
XX	XX	05-SEP-2002 (first entry)	
XX	XX		
XX	XX	B lymphocyte affinity maturation library peptide #56.	
XX	XX		
XX	XX	B lymphocyte stimulator protein binding protein; BLyS; immune disease;	
XX	XX	allergy; proliferative disease; infectious disease; arteriosclerosis;	
XX	XX	inflammatory disorder; hyperimmunoglobulinaemia; blood clotting;	
XX	XX	ischaemia; graft-versus-host disease; neurodegenerative disease;	
XX	XX	immunosuppressive; nephrotropic; antirheumatic; antiarthritic;	
XX	XX	neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;	
XX	XX	antiaesthetic; anti-allergic; thyromimetic; antianemic; haemostatic;	
XX	XX	dermatological; anti-inflammatory; cardiant; ophthalmological; uropathic;	
XX	XX	antidiabetic; antithyroid; antidepressant; hepatotropic.	
XX	XX		
XX	XX	Unidentified.	
XX	XX		
XX	XX	WO200216411-A2.	

XX 28-FEB-2002.  
XX  
XX 17-AUG-2001; 2001WO-US025850.  
PF  
XX 18-AUG-2000; 2000US-0226700P.  
PR  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX Belzter JP, Potter DM, Fleming TL, Rosen CA;  
PI  
XX WPI; 2002-499775/53.  
DR  
XX  
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.  
PS  
XX Claim 70; Page 215; 387pp; English.  
XX  
XX The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (BLyS), BLyS receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of BLyS binding polypeptide.  
CC The BLyS binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of haematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
XX Sequence 14 AA;  
SQ  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 WYDPLTKLWL 10  
Db 3 WYDPLTKLWL 12  
RESULT 83  
AB000787 ID AB000787 standard; peptide; 14 AA.  
XX  
XX AB000787;  
AC  
XX  
XX 05-SEP-2002 (first entry)  
DT  
XX  
XX B lymphocyte affinity maturation library peptide #61.  
DE  
XX  
XX B lymphocyte stimulator protein binding protein; BLyS; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
KW antiaslathmatic; antiallergic; thyromimetic; antianemic; haemostatic;  
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
XX Unidentified.  
OS  
XX  
XX WO200216411-A2.  
PN  
XX  
XX 28-FEB-2002.  
PD  
XX  
XX 17-AUG-2001; 2001WO-US025850.  
PF  
XX  
XX 18-AUG-2000; 2000US-0226700P.  
PR  
XX

PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Belzter JP, Potter DM, Fleming TL, Rosen CA;  
PI  
XX WPI; 2002-499775/53.  
DR  
XX  
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.  
PS  
XX Claim 70; Page 215; 387pp; English.  
XX  
XX The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (BLyS), BLyS receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of BLyS binding polypeptide.  
CC The BLyS binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of haematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
XX Sequence 14 AA;  
SQ  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 WYDPLTKLWL 10  
Db 3 WYDPLTKLWL 12  
RESULT 84  
AB000788 ID AB000788 standard; peptide; 14 AA.  
XX  
XX AB000788;  
AC  
XX  
XX 05-SEP-2002 (first entry)  
DT  
XX  
XX B lymphocyte affinity maturation library peptide #62.  
DE  
XX  
XX B lymphocyte stimulator protein binding protein; BLyS; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
KW antiaslathmatic; antiallergic; thyromimetic; antianemic; haemostatic;  
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
XX Unidentified.  
OS  
XX  
XX WO200216411-A2.  
PN  
XX  
XX 28-FEB-2002.  
PD  
XX  
XX 17-AUG-2001; 2001WO-US025850.  
PF  
XX  
XX 18-AUG-2000; 2000US-0226700P.  
PR  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX  
XX Belzter JP, Potter DM, Fleming TL, Rosen CA;  
PI  
XX  
XX WPI; 2002-499775/53.  
DR  
XX  
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises



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XX  
PS Claim 70; Page 215; 387pp; English.  
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CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of Blys binding polypeptide.  
CC The Blys binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of haematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
SQ Sequence 14 AA;  
  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 WYDPLTKLML 10  
| | | | | | | |  
3 WYDPLTKLML 12  
DB  
  
RESULT 85  
ABJ00807  
ID ABJ00807 standard; peptide; 14 AA.  
XX  
AC ABJ00807;  
XX  
DT 05-SEP-2002 (first entry)  
XX  
DE B lymphocyte affinity maturation library peptide #81.  
XX  
KW B lymphocyte stimulator protein binding protein; Blys; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
KW antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;  
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
OS Unidentified.  
XX  
PN WO200216411-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 17-AUG-2001; 2001WO-US025850.  
XX  
PR 18-AUG-2000; 2000US-0226700P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
XX  
DR WPI; 2002-499775/53.  
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CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of haematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
SQ Sequence 14 AA;  
  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 WYDPLTKLML 10  
| | | | | | | |  
3 WYDPLTKLML 12  
DB  
  
RESULT 86  
ABJ00819  
ID ABJ00819 standard; peptide; 14 AA.  
XX  
AC ABJ00819;  
XX  
DT 05-SEP-2002 (first entry)  
XX  
DE B lymphocyte affinity maturation library peptide #93.  
XX  
KW B lymphocyte stimulator protein binding protein; Blys; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
KW antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;  
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
OS Unidentified.  
XX  
PN WO200216411-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 17-AUG-2001; 2001WO-US025850.  
XX  
PR 18-AUG-2000; 2000US-0226700P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
XX  
DR WPI; 2002-499775/53.  
XX  
PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.  
XX  
PS Claim 70; Page 215; 387pp; English.  
XX  
CC The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of Blys binding polypeptide.  
CC The Blys binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of haematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,

CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
DB 3 WYDPLTKLWL 12

RESULT 87

ID ABJ00838 standard; peptide; 14 AA.

XX ABJ00838;

XX 05-SEP-2002 (first entry)

DE B lymphocyte affinity maturation library peptide #112.

KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
KW antiaesthetic; antiallergic; thyromimetic; antianaemic; haemostatic;  
KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.

XX Unidentified.

XX WO200216411-A2.

XX 28-FEB-2002.

XX 17-AUG-2001; 2001WO-US025850.

XX 18-AUG-2000; 2000US-0226700P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Belzner JP, Potter DM, Fleming TL, Rosen CA;

XX WPI; 2002-499775/53.

PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.

PS Claim 70; Page 216; 387pp; English.

CC The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of BlyS binding polypeptide.  
CC The BlyS binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
DB 3 WYDPLTKLWL 12

RESULT 88

ID ABJ00751 standard; peptide; 14 AA.

XX ABJ00751;

XX 05-SEP-2002 (first entry)

DE B lymphocyte affinity maturation library peptide #25.

KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
KW antiaesthetic; antiallergic; thyromimetic; antianaemic; haemostatic;  
KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.

XX Unidentified.

XX WO200216411-A2.

XX 28-FEB-2002.

XX 17-AUG-2001; 2001WO-US025850.

XX 18-AUG-2000; 2000US-0226700P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Belzner JP, Potter DM, Fleming TL, Rosen CA;

XX WPI; 2002-499775/53.

PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.

PS Claim 70; Page 214; 387pp; English.

CC The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of BlyS binding polypeptide.  
CC The BlyS binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
DB 3 WYDPLTKLWL 12

RESULT 99  
ABJ00767 standard; peptide; 14 AA.  
ID ABJ00767;  
AC ABJ00767;  
XX  
XX  
DT 05-SEP-2002 (first entry)  
XX  
XX B lymphocyte affinity maturation library peptide #41.  
XX  
XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neutroprotective; cytostatic; immunostimulant; antitumor; anti-HIV;  
KW antiasthmatic; antiallergic; thyromimetic; antianaemic; haemostatic;  
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
XX OS Unidentified.  
XX  
XX WO200216411-A2.  
XX  
XX PD 28-FEB-2002.  
XX  
XX PF 17-AUG-2001; 2001WO-US025850.  
XX  
XX PR 18-AUG-2000; 2000US-0226700P.  
XX  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
XX  
XX DR WPI; 2002-499775/53.  
XX  
XX PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.  
XX  
XX PS Claim 70; Page 214; 387pp; English.  
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CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of BlyS binding polypeptide.  
CC The BlyS binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
XX SQ Sequence 14 AA;  
XX  
XX Query Match 100.0%; Score 64; DB 5; Length 14;  
XX Best Local Similarity 100.0%; Pred. No. 0.00094;  
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 05-SEP-2002 (first entry)  
XX  
XX DE B lymphocyte affinity maturation library peptide #58.  
XX  
XX KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neutroprotective; cytostatic; immunostimulant; antitumor; anti-HIV;  
KW antiasthmatic; antiallergic; thyromimetic; antianaemic; haemostatic;  
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
XX OS Unidentified.  
XX  
XX PN WO200216411-A2.  
XX  
XX PD 28-FEB-2002.  
XX  
XX PF 17-AUG-2001; 2001WO-US025850.  
XX  
XX PR 18-AUG-2000; 2000US-0226700P.  
XX  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
XX  
XX DR WPI; 2002-499775/53.  
XX  
XX PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.  
XX  
XX PS Claim 70; Page 215; 387pp; English.  
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CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of BlyS binding polypeptide.  
CC The BlyS binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
XX SQ Sequence 14 AA;  
XX  
XX Query Match 100.0%; Score 64; DB 5; Length 14;  
XX Best Local Similarity 100.0%; Pred. No. 0.00094;  
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 91  
ABJ00795 standard; peptide; 14 AA.  
ID ABJ00795;  
AC ABJ00795;  
XX  
XX  
DT 05-SEP-2002 (first entry)  
XX  
XX DE B lymphocyte affinity maturation library peptide #69.  
XX  
XX KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;

ischaemia; graft-versus-host disease; neurodegenerative disease;  
immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
antiaesthetic; antiallergic; thyromimetic; antianaemic; haemostatic;  
dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
OS Unidentified.  
XX  
XX WO200216411-A2.  
XX  
XX 28-FEB-2002.  
XX  
XX 17-AUG-2001; 2001WO-US025850.  
XX  
XX 18-AUG-2000; 2000US-0226700P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
XX WPI; 2002-499775/53.  
XX  
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XX of haematopoietic origin; or proliferative disease; and reducing,  
XX inhibiting or stimulating immunoglobulin production, B cell proliferation  
XX and graft rejection involving administration of Blys binding polypeptide.  
XX The Blys binding polypeptides are used in the treatment, prevention or  
XX amelioration of diseases such as immune system diseases, proliferative  
XX diseases, diseases of cells of hematopoietic origin, graft rejection,  
XX allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
XX hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
XX neurodegenerative diseases. The present sequence is a B lymphocyte  
XX stimulator protein binding peptide  
XX  
SQ Sequence 14 AA;  
XX  
XX Query Match 100.0%; Score 64; DB 5; Length 14;  
XX Best Local Similarity 100.0%; Pred. No. 0.00094;  
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WYDPLTKLWL 10  
Db 3 WYDPLTKLWL 12  
XX  
XX RESULT 92  
XX ABJ00804  
XX ID ABJ00804 standard; peptide; 14 AA.  
XX  
XX AC ABJ00804;  
XX  
XX DT 05-SEP-2002 (first entry)  
XX  
XX DE B lymphocyte affinity maturation library peptide #78.  
XX  
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;  
XX allergy; proliferative disease; infectious disease; arteriosclerosis;  
XX inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
XX ischaemia; graft-versus-host disease; neurodegenerative disease;  
XX immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
XX neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
XX antiaesthetic; antiallergic; thyromimetic; antianaemic; haemostatic;  
XX dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
XX antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX

OS Unidentified.  
XX  
XX WO200216411-A2.  
XX  
XX 28-FEB-2002.  
XX  
XX 17-AUG-2001; 2001WO-US025850.  
XX  
XX 18-AUG-2000; 2000US-0226700P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
XX WPI; 2002-499775/53.  
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XX of haematopoietic origin; or proliferative disease; and reducing,  
XX inhibiting or stimulating immunoglobulin production, B cell proliferation  
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XX allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
XX hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
XX neurodegenerative diseases. The present sequence is a B lymphocyte  
XX stimulator protein binding peptide  
XX  
SQ Sequence 14 AA;  
XX  
XX Query Match 100.0%; Score 64; DB 5; Length 14;  
XX Best Local Similarity 100.0%; Pred. No. 0.00094;  
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WYDPLTKLWL 10  
Db 3 WYDPLTKLWL 12  
XX  
XX RESULT 93  
XX ABJ00820  
XX ID ABJ00820 standard; peptide; 14 AA.  
XX  
XX AC ABJ00820;  
XX  
XX DT 05-SEP-2002 (first entry)  
XX  
XX DE B lymphocyte affinity maturation library peptide #94.  
XX  
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;  
XX allergy; proliferative disease; infectious disease; arteriosclerosis;  
XX inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
XX ischaemia; graft-versus-host disease; neurodegenerative disease;  
XX immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
XX neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
XX antiaesthetic; antiallergic; thyromimetic; antianaemic; haemostatic;  
XX dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
XX antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
XX OS Unidentified.  
XX  
XX WO200216411-A2.  
XX  
XX 28-FEB-2002.  
XX  
XX 17-AUG-2001; 2001WO-US025850.  
XX  
XX PF

XX 18-AUG-2000; 2000US-0226700P.  
PR (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
XX WPI; 2002-499775/53.  
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XX Claim 70; Page 216; 387pp; English.  
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CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving immunoglobulin production of Blys binding polypeptide.  
CC The Blys binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
XX Sequence 14 AA;  
SQ  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WYDPLTKLML 10  
|||  
3 WYDPLTKLML 12  
Db  
RESULT 94  
ABJ00828  
ID ABJ00828 standard; peptide; 14 AA.  
XX  
XX ABJ00828;  
AC  
XX  
XX 05-SEP-2002 (first entry)  
DT  
XX  
XX B lymphocyte affinity maturation library peptide #102.  
DE  
XX  
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
KW antiaesthetic; anti-allergic; thymomimetic; antianemic; haemostatic;  
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
XX Unidentified.  
OS  
XX WO200216411-A2.  
PN  
XX 28-FEB-2002.  
PD  
XX 17-AUG-2001; 2001WO-US025850.  
PF  
XX 18-AUG-2000; 2000US-0226700P.  
PR (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
XX

DR WPI; 2002-499775/53.  
XX  
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.  
XX  
XX Claim 70; Page 216; 387pp; English.  
XX  
XX The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving immunoglobulin production of Blys binding polypeptide.  
CC The Blys binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
XX Sequence 14 AA;  
SQ  
Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WYDPLTKLML 10  
|||  
3 WYDPLTKLML 12  
Db  
RESULT 95  
ABJ00734  
ID ABJ00734 standard; peptide; 14 AA.  
XX  
XX ABJ00734;  
AC  
XX  
XX 05-SEP-2002 (first entry)  
DT  
XX  
XX B lymphocyte affinity maturation library peptide #8.  
DE  
XX  
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
KW antiaesthetic; anti-allergic; thymomimetic; antianemic; haemostatic;  
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
XX  
XX Unidentified.  
OS  
XX WO200216411-A2.  
PN  
XX 28-FEB-2002.  
PD  
XX 17-AUG-2001; 2001WO-US025850.  
PF  
XX 18-AUG-2000; 2000US-0226700P.  
PR (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
XX  
XX WPI; 2002-499775/53.  
DR  
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises  
PT administering B lymphocyte stimulator binding polypeptide.  
XX  
XX Claim 70; Page 214; 387pp; English.  
XX

The present invention relates to the treatment, prevention or amelioration of a disease or disorder associated with: aberrant B lymphocyte stimulator (Blys), Blys receptor expression or activity; cells of hematopoietic origin; or proliferative diseases; and reducing, inhibiting or stimulating immunoglobulin production, B cell proliferation and graft rejection involving administration of Blys binding polypeptide. The Blys binding polypeptides are used in the treatment, prevention or amelioration of diseases such as immune system diseases, proliferative diseases, diseases of cells of hematopoietic origin, graft rejection, allergies, infectious diseases, arteriosclerosis, inflammatory disorders, hypergammaglobulinaemia, blood clotting disorders, ischemia, and neurodegenerative diseases. The present sequence is a B Lymphocyte stimulator protein binding peptide

Sequence 14 AA:

Query Match	100.0%	Score 64	DB 5	Length 14
Best Local Similarity	100.0%	Pred. No.	0.00094	
Match 10, Conservative	0	Mismatches	0	Indels 0
				Gaps 0

QY	1	WYDPLTKLWL	10
Db	3	WYDPLTKLWL	12

RESULT 96  
ABJ00743

ID ABJ00743 standard; peptide; 14 AA.

AC ABJ00743;

DT 05-SEP-2002 (first entry)

B lymphocyte affinity maturation library peptide #17.

B lymphocyte stimulator protein binding protein; BMy; immune disease; allergy; proliferative disease; infectious disease; arteriosclerosis; inflammatory disorder; hypermaglobulinemia; blood clotting; ischaemia; graft-versus-host disease; neurodegenerative disease; immunosuppressive; nephrotropic; antineuritic; antitachyitic; neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV; antiasmatic; antiallergic; thyromimetic; antianemic; haemostatic; dermatological; antinflammatory; cardiant; ophthalmological; uropathic; antidiabetic; antihypertoid; antidepressant; hepatotropic.

Unidentified.

AA WO200216411-A2.  
PN

XX  
PD 28-FEB-2002.

17-AUG-2001; 2001WO-US025850.

AA  
PR 18-AUG-2000; 2000US-0226700P.

XX  
PA (HIMA-) HUMAN GENOME SCI INC.

XX Bel'tzer JP, Potter DM, Fleming TL, Rosen CA;  
PT

XX WPB : 2002-499775/53.  
DB

PT The treatment of various diseases e.g. rheumatoid arthritis, comprises administering B lymphocyte stimulator binding polypeptide.

xx  
PS  
Claim 70: Page 214: 387pp: English.

The present invention relates to the treatment, prevention or amelioration of a disease or disorder associated with: aberrant B lymphocyte stimulator (Blys), Blys receptor expression or activity; cells of haematopoietic origin; or proliferative disease; and reducing, inhibiting or stimulating immunoglobulin production, B cell proliferation and graft rejection involving administration of Blys binding polypeptide. The Blys binding polypeptides are used in the treatment, prevention or

amelioration of diseases such as immune system diseases, proliferative diseases, diseases of cells of hematopoietic origin, graft rejection, allergies, infectious diseases, arteriosclerosis, inflammatory disorders hypergammaglobulinaemia, blood clotting disorders, ischaemia, and neurodegenerative diseases. The present sequence is a B lymphocyte stimulator protein binding peptide

**SQ** Sequence 14 AA;

Query Match	100.0%	Score 64;	DB 5;	Length 14;
Best Local Similarity	100.0%	Pred. No. 0.00094;		
Matches 10; Conservative	0;	Mismatches	0;	Gaps 0;

QY 1 WYDPLTKLWL 10  
Db 3 WYDPLTKLWL 12

## RESULT 97

ABJ00745 standard; peptide; 14 AA.

AC ABJ00745;

AA DT 05-SEP-2002 (first entry)

XX B lymphocyte affinity maturation library peptide #19.  
DE

XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antineuritic; antiarthritic;  
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
KW antineoplastic; antiallergic; thyromimetic; antinaemic; hemostatic;  
KW dermatologic; antinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; anticholinergic; antidepressant; hepatotropic;  
KW

xx  
OS  
unidentified.

XX  
PN W0200216411-A2.

XX PD 28-FEB-2002.

XX  
DE 17-ATIG-2001 : 2001WO-IIS025850.

18-AUG-2000: 2000UTS-0226700P.

XX  
DA  
(HITMA-) HITMAN GENOME SCT INC

XX  
Dolan TB  
Dotter DM  
Fleming TT  
Rosen CA:

XX  
XX  
WDT - 0003 - 40077E/E3  
DT

XX PT The treatment of various diseases e.g. rheumatoid arthritis, comprises administering B lymphocyte stimulator binding polypeptide.

XX  
XX  
C1ajm 70: Page 214: 387pm: English.

AA The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of Blys binding polypeptide.  
CC The Blys binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of haematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide

SO Sequence 14 AA; Score 64; DB 5; Length 14;  
Query Match 100.0%; Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10  
3 WYDPLTKLML 12

DB 3 WYDPLTKLML 12

RESULT 98  
ABJ00759  
ID ABJ00759 standard; peptide; 14 AA.  
AC ABJ00759;  
DT 05-SEP-2002 (first entry)

XX B lymphocyte affinity maturation library peptide #33.  
XX  
XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;  
KW antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;  
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.

XX Unidentified.  
XX  
XX WO200216411-A2.  
XX PN  
XX 28-FEB-2002.  
XX PD  
XX 17-AUG-2001; 2001WO-US025850.  
XX PF  
XX 18-AUG-2000; 2000US-0226700P.  
XX PR  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX PA  
XX  
XX PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
XX  
XX WPI; 2002-499775/53.  
XX DR  
XX  
XX PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
XX administering B lymphocyte stimulator binding polypeptide.  
XX  
XX  
XX Claim 70; Page 214; 387pp; English.  
XX  
XX The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of BlyS binding polypeptide.  
CC The BlyS binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of haematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
XX  
XX Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10  
3 WYDPLTKLML 12

DB 3 WYDPLTKLML 12

RESULT 99  
ABJ00778  
ID ABJ00778 standard; peptide; 14 AA.  
XX  
XX  
XX AC ABJ00778;  
XX  
XX DT 05-SEP-2002 (first entry)

XX B lymphocyte affinity maturation library peptide #52.  
XX  
XX  
XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
KW neuroprotective; cyostatic; immunostimulant; antitumour; anti-HIV;  
KW antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;  
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.

XX Unidentified.  
XX  
XX WO200216411-A2.  
XX PN  
XX 28-FEB-2002.  
XX PD  
XX 17-AUG-2001; 2001WO-US025850.  
XX PF  
XX 18-AUG-2000; 2000US-0226700P.  
XX PR  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX PA  
XX  
XX PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
XX  
XX WPI; 2002-499775/53.  
XX DR  
XX  
XX PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
XX administering B lymphocyte stimulator binding polypeptide.  
XX  
XX  
XX Claim 70; Page 215; 387pp; English.  
XX  
XX The present invention relates to the treatment, prevention or  
CC amelioration of a disease or disorder associated with: aberrant B  
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells  
CC of haematopoietic origin; or proliferative disease; and reducing,  
CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
CC and graft rejection involving administration of BlyS binding polypeptide.  
CC The BlyS binding polypeptides are used in the treatment, prevention or  
CC amelioration of diseases such as immune system diseases, proliferative  
CC diseases, diseases of cells of haematopoietic origin, graft rejection,  
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
CC neurodegenerative diseases. The present sequence is a B lymphocyte  
CC stimulator protein binding peptide  
XX  
XX  
XX Sequence 14 AA;

Query Match 100.0%; Score 64; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10  
3 WYDPLTKLML 12

DB 3 WYDPLTKLML 12

RESULT 100  
ABJ00796  
ID ABJ00796 standard; peptide; 14 AA.

XX ABQ00796;  
 AC  
 XX  
 DT 05-SEP-2002 (first entry)  
 DE  
 XX  
 DE B lymphocyte affinity maturation library peptide #70.  
 XX  
 KW B lymphocyte stimulator protein binding protein; BLyS; immune disease;  
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
 KW immunosuppressive; nephrotropic; antineumatic; antiarthritic;  
 KW neuropsychiatric; cytosolic; immunostimulant; antitumor; anti-HIV;  
 KW antidiabetic; antiallergic; thymic; antianemic; haemostatic;  
 KW dermatological; antineoplastic; cardiant; ophthalmological; uropathic;  
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200216411-A2.  
 PD  
 XX 28-FEB-2002.  
 PF  
 XX 17-AUG-2001; 2001WO-US025850.  
 PR 18-AUG-2000; 2000US-0226700P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI Belzer JP, Potter DM, Fleming TL, Rosen CA;  
 DR WPI; 2002-499775/53.  
 XX  
 PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
 XX administering B lymphocyte stimulator binding polypeptide.  
 PS Claim 70; Page 215; 387pp; English.  
 XX  
 CC The present invention relates to the treatment, prevention or  
 CC amelioration of a disease or disorder associated with: aberrant B  
 CC lymphocyte stimulator (BLyS), BLyS receptor expression or activity; cells  
 CC of haematopoietic origin; or proliferative disease; and reducing,  
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
 CC and graft rejection involving administration of BLyS binding polypeptide.  
 CC The BLyS binding polypeptides are used in the treatment, prevention or  
 CC amelioration of diseases such as immune system diseases, proliferative  
 CC diseases, diseases of cells of haematopoietic origin, graft rejection,  
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
 CC neurodegenerative diseases. The present sequence is a B lymphocyte  
 CC stimulator protein binding peptide  
 XX  
 SQ Sequence 14 AA;  
 QY Query Match 100.0%; Score 64; DB 5; Length 14;  
 DB Best Local Similarity 100.0%; Pred. No. 0.00094; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 WYDPLTKLWL 10  
 3 WYDPLTKLWL 12

Search completed: July 12, 2004, 21:28:48  
 Job time : 55 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 12, 2004, 21:23:57 ; Search time 23 Seconds  
(without alignments)  
22.446 Million cell updates/sec

Title: US-09-932-613-457  
Perfect score: 64  
Sequence: 1 WYDPLTKML 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 300 summaries

Database : Issued Patents AA: \*  
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5: /cgn2\_6/ptodata/2/1aa/PCTUS.COMB.pep: \*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	68.8	52	4	US-09-621-976-7356
2	42	65.6	49	4	US-09-636-791A-18
3	42	65.6	619	4	US-09-636-791A-15
4	42	65.6	642	4	US-09-337-307A-3
5	42	65.6	642	4	US-09-337-307A-4
6	41	64.1	593	4	US-09-328-352-4866
7	41	64.1	685	4	US-09-252-991A-31711
8	39	60.9	193	4	US-09-489-039A-12391
9	39	60.9	410	4	US-09-489-039A-9029
10	39	60.9	727	3	US-09-179-558-56
11	39	60.9	727	4	US-09-722-825-56
12	39	60.9	727	4	US-09-722-487-56
13	39	60.9	727	4	US-09-722-708-56
14	39	60.9	941	3	US-09-179-558-55
15	39	60.9	941	3	US-09-722-825-55
16	39	60.9	941	4	US-09-722-487-55
17	39	60.9	941	4	US-09-722-708-55
18	38	59.4	345	4	US-09-252-991A-21042
19	38	59.4	780	4	US-09-328-352-8180
20	37.5	58.6	301	1	US-08-674-168-31
21	37.5	58.6	301	3	US-08-985-908-15
22	37.5	58.6	301	3	US-08-852-730-20
23	37	57.8	79	4	US-09-328-352-8223
24	37	57.8	93	4	US-09-621-976-6153
25	37	57.8	158	4	US-09-834-759-508
26	37	57.8	243	4	US-09-834-759-507
27	37	57.8	311	4	US-09-489-039A-8990

28	37	57.8	383	3	US-09-041-718-3	Sequence 3, Appli
29	37	57.8	437	4	US-09-328-352-5102	Sequence 5102, Ap
30	37	57.8	819	4	US-09-976-834-369	Sequence 369, App
31	37	57.8	985	2	US-08-660-326-41	Sequence 41, Appl
32	36	56.2	308	2	US-08-164-292B-18	Sequence 18, Appl
33	36	56.2	308	3	US-08-845-623-18	Sequence 18, Appl
34	36	56.2	308	3	US-08-815-927-18	Sequence 18, Appl
35	36	56.2	308	4	US-09-103-330-18	Sequence 18, Appl
36	36	56.2	308	4	US-09-435-242-18	Sequence 18, Appl
37	36	56.2	321	4	US-09-688-019-2	Sequence 2, Appli
38	36	56.2	364	4	US-09-543-661A-5748	Sequence 5748, Ap
39	36	56.2	399	4	US-09-491-577-36	Sequence 36, Appl
40	36	56.2	402	4	US-09-134-000C-4382	Sequence 4382, Ap
41	36	56.2	430	4	US-09-107-532A-6726	Sequence 6726, Ap
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48	36	56.2	700	5	PCT-US95-08560-2	Sequence 2, Appli
49	36	56.2	713	4	US-09-540-236-3595	Sequence 3595, Ap
50	36	56.2	842	4	US-09-688-1888-91	Sequence 91, Appl
51	36	56.2	842	4	US-09-291-417D-91	Sequence 91, Appl
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54	35	54.7	220	4	US-09-252-991A-20618	Sequence 20618, A
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57	35	54.7	359	3	US-09-374-493-11	Sequence 11, Appl
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59	35	54.7	359	3	US-09-374-492-11	Sequence 11, Appl
60	35	54.7	359	3	US-09-785-343-11	Sequence 11, Appl
61	35	54.7	361	4	US-09-724-566A-75	Sequence 75, Appl
62	35	54.7	374	4	US-09-724-566A-71	Sequence 71, Appl
63	35	54.7	390	4	US-09-724-566A-70	Sequence 70, Appl
64	35	54.7	395	4	US-09-724-566A-68	Sequence 68, Appl
65	35	54.7	407	4	US-09-724-566A-58	Sequence 58, Appl
66	35	54.7	419	4	US-09-724-566A-57	Sequence 57, Appl
67	35	54.7	420	4	US-09-724-566A-60	Sequence 60, Appl
68	35	54.7	424	4	US-08-879-337-5	Sequence 5, Appli
69	35	54.7	425	4	US-09-548-372D-28	Sequence 28, Appl
70	35	54.7	425	4	US-09-548-367D-28	Sequence 28, Appl
71	35	54.7	425	4	US-09-551-853D-28	Sequence 28, Appl
72	35	54.7	428	4	US-09-548-372D-51	Sequence 51, Appl
73	35	54.7	428	4	US-09-548-367D-51	Sequence 51, Appl
74	35	54.7	428	4	US-09-551-853D-51	Sequence 51, Appl
75	35	54.7	431	4	US-09-724-566A-74	Sequence 74, Appl
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77	35	54.7	433	4	US-09-548-367D-26	Sequence 26, Appl
78	35	54.7	433	4	US-09-551-853D-26	Sequence 26, Appl
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80	35	54.7	434	4	US-09-548-367D-53	Sequence 53, Appl
81	35	54.7	434	4	US-09-551-853D-53	Sequence 53, Appl
82	35	54.7	439	4	US-09-724-566A-67	Sequence 67, Appl
83	35	54.7	444	4	US-09-724-566A-67	Sequence 67, Appl
84	35	54.7	446	4	US-09-548-372D-22	Sequence 22, Appl
85	35	54.7	446	4	US-09-548-367D-22	Sequence 22, Appl
86	35	54.7	446	4	US-09-551-853D-22	Sequence 22, Appl
87	35	54.7	449	4	US-09-230-371A-28	Sequence 28, Appl
88	35	54.7	452	4	US-09-724-566A-58	Sequence 58, Appl
89	35	54.7	453	4	US-09-548-372D-30	Sequence 30, Appl
90	35	54.7	453	4	US-09-548-367D-30	Sequence 30, Appl
91	35	54.7	453	4	US-09-551-853D-30	Sequence 30, Appl
92	35	54.7	456	4	US-09-724-566A-43	Sequence 43, Appl
93	35	54.7	459	4	US-09-548-372D-24	Sequence 24, Appl
94	35	54.7	459	4	US-09-548-372D-32	Sequence 32, Appl
95	35	54.7	459	4	US-09-548-367D-24	Sequence 24, Appl
96	35	54.7	459	4	US-09-548-372D-32	Sequence 32, Appl
97	35	54.7	459	4	US-09-551-853D-24	Sequence 24, Appl
98	35	54.7	459	4	US-09-551-853D-32	Sequence 32, Appl
99	35	54.7	476	4	US-09-548-372D-6	Sequence 6, Appli
100	35	54.7	476	4	US-09-548-372D-73	Sequence 73, Appl



247 33 51.6 3672 4 US-09-396-540-12 Sequence 12, Appl  
248 33 51.6 3801 2 US-08-822-445-10 Sequence 10, Appl  
249 33 51.6 3801 4 US-09-396-540-10 Sequence 10, Appl  
250 32.5 50.8 505 4 US-09-291-541-10 Sequence 10, Appl  
251 32.5 50.8 542 4 US-09-198-452A-96 Sequence 496, App  
252 32 50.0 15 4 US-09-069-827A-128 Sequence 128, App  
253 32 50.0 38 4 US-09-252-586-26 Sequence 26, Appl  
254 32 50.0 100 3 US-08-881-037-39 Sequence 39, Appl  
255 32 50.0 113 2 US-08-428-197-46 Sequence 46, Appl  
256 32 50.0 113 2 PCT-US93-10555-46 Sequence 46, Appl  
257 32 50.0 197 4 US-09-328-352-6087 Sequence 6087, App  
258 32 50.0 226 2 US-08-924-759-4 Sequence 4, Appl  
259 32 50.0 226 3 US-09-248-335-4 Sequence 4, Appl  
260 32 50.0 230 3 US-09-248-335-44 Sequence 22, Appl  
261 32 50.0 265 4 US-09-454-279-22 Sequence 22, Appl  
262 32 50.0 293 4 US-09-134-001C-5374 Sequence 5374, App  
263 32 50.0 315 3 US-09-135-639-4 Sequence 4, Appl  
264 32 50.0 316 4 US-09-328-352-6294 Sequence 6294, App  
265 32 50.0 322 4 US-09-489-039A-13138 Sequence 13138, A  
266 32 50.0 334 1 US-08-347-826A-2 Sequence 2, Appl  
267 32 50.0 334 4 US-09-463-702A-38 Sequence 38, Appl  
268 32 50.0 334 4 US-09-699-135-38 Sequence 38, Appl  
269 32 50.0 335 1 US-08-347-826A-1 Sequence 1, Appl  
270 32 50.0 360 2 US-08-459-346-13 Sequence 13, Appl  
271 32 50.0 360 2 US-08-411-607A-4 Sequence 4, Appl  
272 32 50.0 360 3 US-08-889-419-13 Sequence 13, Appl  
273 32 50.0 360 4 US-08-402-542-13 Sequence 13, Appl  
274 32 50.0 360 4 US-09-361-741-4 Sequence 4, Appl  
275 32 50.0 360 5 PCT-US93-07189-13 Sequence 13, Appl  
276 32 50.0 370 2 US-08-559-303B-77 Sequence 77, Appl  
277 32 50.0 370 3 US-09-175-828-77 Sequence 77, Appl  
278 32 50.0 374 1 US-08-464-148-2 Sequence 2, Appl  
279 32 50.0 374 1 US-08-385-500-2 Sequence 2, Appl  
280 32 50.0 374 1 US-08-846-784-2 Sequence 2, Appl  
281 32 50.0 386 4 US-09-252-991A-30688 Sequence 30688, A  
282 32 50.0 391 4 US-09-252-991A-16745 Sequence 16745, A  
283 32 50.0 454 3 US-08-929-329-8 Sequence 8, Appl  
284 32 50.0 454 3 US-09-306-593-9 Sequence 9, Appl  
285 32 50.0 513 4 US-09-351-229-4 Sequence 4, Appl  
286 32 50.0 520 4 US-09-252-991A-30677 Sequence 30677, A  
287 32 50.0 527 4 US-09-930-218-16 Sequence 16, Appl  
288 32 50.0 530 4 US-09-252-586-2 Sequence 2, Appl  
289 32 50.0 531 3 US-08-688-988-38 Sequence 38, Appl  
290 32 50.0 532 3 US-09-181-336-15 Sequence 15, Appl  
291 32 50.0 543 2 US-08-922-170B-10 Sequence 10, Appl  
292 32 50.0 543 3 US-09-071-739B-2 Sequence 2, Appl  
293 32 50.0 543 3 US-09-181-336-13 Sequence 13, Appl  
294 32 50.0 543 4 US-09-260-038B-2 Sequence 2, Appl  
295 32 50.0 543 4 US-09-739-455-4 Sequence 4, Appl  
296 32 50.0 543 4 US-09-739-455-14 Sequence 14, Appl  
297 32 50.0 543 4 US-09-635-923-2 Sequence 2, Appl  
298 32 50.0 543 4 US-09-487-716A-2 Sequence 2, Appl  
299 32 50.0 543 4 US-09-322-977-2 Sequence 2, Appl  
300 32 50.0 543 4

## ALIGNMENTS

RESULT 1  
US-09-621-976-7356  
Sequence 7356, Application US/09621976  
Patent No. 6639063  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Jobert, S.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
FILE REFERENCE: GENSET.054PR2  
CURRENT APPLICATION NUMBER: US/09/621,976  
CURRENT FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm

SEQ ID NO 7356  
LENGTH: 52  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-621-976-7356

Query Match 68.8%; Score 44; DB 4; Length 52;  
Best Local Similarity 55.6%; Pred. No. 1.6;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9  
|||:|:  
Db 26 WYTPNKKLM 34

RESULT 2  
US-09-636-791A-18  
Sequence 18, Application US/09636791A  
Patent No. 6503703  
GENERAL INFORMATION:  
APPLICANT: Palese et al  
TITLE OF INVENTION: IDENTIFICATION AND USE OF ANTIVIRAL COMPOUNDS THAT  
INHIBIT INTERACTION OF HOST CELL PROTEINS AND VIRAL  
FILE REFERENCE: 6923-077-999  
CURRENT APPLICATION NUMBER: US/09/636,791A  
CURRENT FILING DATE: 2000-08-11  
PRIOR APPLICATION NUMBER: 60/148,263  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 18  
LENGTH: 49  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-636-791A-18

Query Match 65.6%; Score 42; DB 4; Length 49;  
Best Local Similarity 75.0%; Pred. No. 3.3;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9  
|||:|:  
Db 22 FDPVTKLM 29

RESULT 3  
US-09-636-791A-15  
Sequence 15, Application US/09636791A  
Patent No. 6503703  
GENERAL INFORMATION:  
APPLICANT: Palese et al  
TITLE OF INVENTION: IDENTIFICATION AND USE OF ANTIVIRAL COMPOUNDS THAT  
INHIBIT INTERACTION OF HOST CELL PROTEINS AND VIRAL  
FILE REFERENCE: 6923-077-999  
CURRENT APPLICATION NUMBER: US/09/636,791A  
CURRENT FILING DATE: 2000-08-11  
PRIOR APPLICATION NUMBER: 60/148,263  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 619  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-636-791A-15

Query Match 65.6%; Score 42; DB 4; Length 619;  
Best Local Similarity 75.0%; Pred. No. 42;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9

Db 485 FDPVTKLM 492

RESULT 4

US-09-337-307A-3  
; Sequence 3, Application US/09337307A  
; Patent No. 6432692  
; GENERAL INFORMATION:  
; APPLICANT: Bradford, Christopher A.  
; APPLICANT: Carver, Lucy A.  
; APPLICANT: Dunham, Elizabeth E.  
; TITLE OF INVENTION: Sensitive Biosay For Detecting Agonists Of The Aryl Hydrocarbon  
; FILE REFERENCE: WARP0105  
; CURRENT APPLICATION NUMBER: US/09/337,307A  
; CURRENT FILING DATE: 1999-06-21  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 642  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: /note = "ARA3"  
US-09-337-307A-3

Query Match 65.6%; Score 42; DB 4; Length 642;  
Best Local Similarity 75.0%; Pred. No. 44;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9  
Db 485 FDPVTKLM 492

RESULT 5

US-09-337-307A-4  
; Sequence 4, Application US/09337307A  
; Patent No. 6432692  
; GENERAL INFORMATION:  
; APPLICANT: Bradford, Christopher A.  
; APPLICANT: Carver, Lucy A.  
; APPLICANT: Dunham, Elizabeth E.  
; TITLE OF INVENTION: Sensitive Biosay For Detecting Agonists Of The Aryl Hydrocarbon  
; FILE REFERENCE: WARP0105  
; CURRENT APPLICATION NUMBER: US/09/337,307A  
; CURRENT FILING DATE: 1999-06-21  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 642  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: /note = "ARA3"  
US-09-337-307A-4

Query Match 65.6%; Score 42; DB 4; Length 642;  
Best Local Similarity 75.0%; Pred. No. 44;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9  
Db 485 FDPVTKLM 492

RESULT 6

US-09-328-352-4866  
; Sequence 4866, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 4866  
; LENGTH: 593  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-4866

Query Match 64.1%; Score 41; DB 4; Length 593;  
Best Local Similarity 66.7%; Pred. No. 59;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLM 10  
Db 49 YDPLNITML 57

RESULT 7

US-09-252-991A-31711  
; Sequence 31711, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 31711  
; LENGTH: 685  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-31711

Query Match 64.1%; Score 41; DB 4; Length 685;  
Best Local Similarity 50.0%; Pred. No. 68;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKML 10  
Db 579 WFDPSGRMLI 588

RESULT 8

US-09-489-039A-12391  
; Sequence 12391, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 12391  
; LENGTH: 193  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-12391

Query Match 60.9%; Score 39; DB 4; Length 193;  
Best Local Similarity 58.3%; Pred. No. 40;  
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 WYD--PLTKLWL 10  
Db 83 WYVSPPLKLMW 94

RESULT 9  
US-09-489-039A-9029

; Sequence 9029, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; PRIOR FILING DATE: 2000-01-27

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 9029

; LENGTH: 410

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-9029

Query Match 60.9%; Score 39; DB 4; Length 410;  
Best Local Similarity 50.0%; Pred. No. 85;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
Db 241 WYDVVCMIMWL 250

RESULT 10  
US-09-179-558-56

; Sequence 56, Application US/09179558

; Patent No. 6180612

; GENERAL INFORMATION:

; APPLICANT: Hockensmith, Joel W.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR

; TARGETING DNA METABOLIC PROCESSES USING

; TITLE OF INVENTION: AMINOGLYCOSIDE DERIVATIVES

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PENNIE & EDMONDS LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/179,558

; FILING DATE: 27-OCT-1998

; CLASSIFICATION: 514

; PRIOR APPLICATION NUMBER: U.S. 09/060,470

; FILING DATE: 15-APR-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. 60/063,898

; FILING DATE: 31-OCT-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 9426-005-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)7909090

TELEFAX: (212)8699741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 56:

SEQUENCE CHARACTERISTICS:

LENGTH: 727 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-179-558-56

QY 2 YDPLTKLW 9  
Db 53 YDPAKTKW 60

RESULT 11  
US-09-722-825-56

; Sequence 56, Application US/09722825

; Patent No. 6531306

; GENERAL INFORMATION:

; APPLICANT: Hockensmith, Joel W.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR

; TARGETING DNA METABOLIC PROCESSES USING

; AMINOGLYCOSIDE DERIVATIVES

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PENNIE & EDMONDS LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/722,825

; FILING DATE: 28-No. 6531306-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/179,558

; FILING DATE: <Unknown>

; APPLICATION NUMBER: U.S. 60/063,898

; FILING DATE: 31-OCT-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 9426-005-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)7909090

; TELEFAX: (212)8699741

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 56:

SEQUENCE CHARACTERISTICS:

LENGTH: 727 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 56:

US-09-722-825-56

Query Match 60.9%; Score 39; DB 4; Length 727;  
Best Local Similarity 75.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKLM 9  
Db 53 YDPATKTM 60

RESULT 12  
US-09-722-487-56  
Sequence 56, Application US/09722487  
Patent No. 6537791  
GENERAL INFORMATION:  
APPLICANT: Hockensmith, Joel W.  
Muthuswami, Rohini  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
TARGETING DNA METABOLIC PROCESSES USING  
AMINOGLYCOSIDE DERIVATIVES  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/722,487  
FILING DATE: 28-NO. 6537791-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/179,558  
FILING DATE: <Unknown>  
APPLICATION NUMBER: U.S. 60/063,898  
FILING DATE: 31-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 9426-005-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)7909090  
TELEFAX: (212)8699741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 727 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 56:  
US-09-722-487-56

Query Match 60.9%; Score 39; DB 4; Length 727;  
Best Local Similarity 75.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKLM 9  
Db 53 YDPATKTM 60

RESULT 13  
US-09-722-708-56  
Sequence 56, Application US/09722708  
Patent No. 6573060

GENERAL INFORMATION:  
APPLICANT: Hockensmith, Joel W.  
Muthuswami, Rohini  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
TARGETING DNA METABOLIC PROCESSES USING  
AMINOGLYCOSIDE DERIVATIVES  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/722,708  
FILING DATE: 28-NO. 6573060-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/179,558  
FILING DATE: <Unknown>  
APPLICATION NUMBER: U.S. 60/063,898  
FILING DATE: 31-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 9426-005-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)7909090  
TELEFAX: (212)8699741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 727 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 56:  
US-09-722-708-56

Query Match 60.9%; Score 39; DB 4; Length 727;  
Best Local Similarity 75.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKLM 9  
Db 53 YDPATKTM 60

RESULT 14  
US-09-179-558-55  
Sequence 55, Application US/09179558  
Patent No. 6180612  
GENERAL INFORMATION:  
APPLICANT: Hockensmith, Joel W.  
Muthuswami, Rohini  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
TARGETING DNA METABOLIC PROCESSES USING  
AMINOGLYCOSIDE DERIVATIVES  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/179,558  
FILING DATE: 27-OCT-1998  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 09/060,470  
FILING DATE: 15-APR-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 60/063,898  
FILING DATE: 31-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 9426-005-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)7909090  
TELEFAX: (212)8699741  
TELLEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 941 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-179-558-55

Query Match 60.9%; Score 39; DB 3; Length 941;  
Best Local Similarity 75.0%; Pred. No. 2e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKLW 9  
Db 267 YDPATKTM 274

RESULT 15  
US-09-722-825-55  
Sequence 55, Application US/09722825  
Patent No. 6531306  
GENERAL INFORMATION:  
APPLICANT: Hockensmith, Joel W.  
Muthuswami, Rohini  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
TARGETING DNA METABOLIC PROCESSES USING  
AMINOGLYCOSIDE DERIVATIVES  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/722,825  
FILING DATE: 28-NO. 6531306-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/179,558  
FILING DATE: <Unknown>  
APPLICATION NUMBER: U.S. 60/063,898  
FILING DATE: 31-OCT-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 9426-005-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)7909090  
TELEFAX: (212)8699741  
TELLEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 941 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 55:  
US-09-722-825-55

Query Match 60.9%; Score 39; DB 4; Length 941;  
Best Local Similarity 75.0%; Pred. No. 2e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKLW 9  
Db 267 YDPATKTM 274

RESULT 16  
US-09-722-487-55  
Sequence 55, Application US/09722487  
Patent No. 6537791  
GENERAL INFORMATION:  
APPLICANT: Hockensmith, Joel W.  
Muthuswami, Rohini  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
TARGETING DNA METABOLIC PROCESSES USING  
AMINOGLYCOSIDE DERIVATIVES  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/722,487  
FILING DATE: 28-NO. 6537791-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/179,558  
FILING DATE: <Unknown>  
APPLICATION NUMBER: U.S. 60/063,898  
FILING DATE: 31-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 9426-005-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)7909090  
TELEFAX: (212)8699741  
TELLEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 941 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 55:  
US-09-722-487-55

Query Match 60.9%; Score 39; DB 4; Length 941;  
Best Local Similarity 75.0%; Pred. No. 2e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9  
Db 267 YDPATKTM 274

RESULT 17  
US-09-722-708-55  
Sequence 55, Application US/09722708  
Patent No. 6573060  
GENERAL INFORMATION:  
APPLICANT: Hockensmith, Joel W.  
Muthuswami, Rohini  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
TARGETING DNA METABOLIC PROCESSES USING  
AMINOGLYCOSIDE DERIVATIVES  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSO Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/722,708  
FILING DATE: 28-NO. 6573060-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/179,558  
FILING DATE: <Unknown>  
APPLICATION NUMBER: U.S. 60/063,898  
FILING DATE: 31-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 9426-005-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)7909090  
TELEFAX: (212)8699741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 941 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 55:  
US-09-722-708-55

Query Match 60.9%; Score 39; DB 4; Length 941;  
Best Local Similarity 75.0%; Pred. No. 2e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9  
Db 267 YDPATKTM 274

RESULT 18

US-09-252-991A-21042  
Sequence 21042, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 21042  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-21042

Query Match 59.4%; Score 38; DB 4; Length 345;  
Best Local Similarity 85.7%; Pred. No. 1e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 DPLTKLM 9  
Db 188 DPLTKLM 194

RESULT 19  
US-09-328-352-8180  
Sequence 8180, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
FILE REFERENCE: GTC99-039A  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 8180  
LENGTH: 780  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-8180

Query Match 59.4%; Score 38; DB 4; Length 780;  
Best Local Similarity 50.0%; Pred. No. 2.4e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKML 10  
Db 647 WYDPRGVLM 656

RESULT 20  
US-08-674-168-31  
Sequence 31, Application US/08674168  
Patent No. 5804414  
GENERAL INFORMATION:  
APPLICANT: MORIYA, Mika  
APPLICANT: MATSUI, Hiroshi  
APPLICANT: YOKOZAKI, Kenzo  
APPLICANT: HIRANO, Seiko  
APPLICANT: HAYAKAWA, Atsushi  
APPLICANT: IZUI, Masako  
APPLICANT: SUGIMOTO, Masakazu  
TITLE OF INVENTION: METHOD OF AMPLIFYING GENE USING  
TITLE OF INVENTION: ARTIFICIAL TRANSPOSON  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:



ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P.C.  
STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/674,168  
FILING DATE: 01-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-166541  
FILING DATE: 30-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-810-0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248655 OPAT UR  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 301 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-674-168-31

Query Match 58.6%; Score 37.5; DB 1; Length 301;  
Best Local Similarity 53.8%; Pred. No. 1.1e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

Qy 1 WY---DPLTKLWL 10  
Db 193 WYSGDDPLNLVWL 205

RESULT 21  
US-08-985-908-15  
Sequence 15, Application US/08985908  
Patent No. 6004773  
GENERAL INFORMATION:  
APPLICANT: MASAYUKI ARAKI, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI NA  
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
CITY: ARLINGTON  
STATE: VA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/985,908  
FILING DATE: 05-DEC-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-325659  
FILING DATE: 05-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: NORMAN F. OBLON

REGISTRATION NUMBER: 24,618  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 301 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-985-908-15

Query Match 58.6%; Score 37.5; DB 3; Length 301;  
Best Local Similarity 53.8%; Pred. No. 1.1e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

Qy 1 WY---DPLTKLWL 10  
Db 193 WYSGDDPLNLVWL 205

RESULT 22  
US-08-852-730-20  
Sequence 20, Application US/08852730  
Patent No. 6090597  
GENERAL INFORMATION:  
APPLICANT: SEIRO HIRANO, MASAKAZU SUGIMOTO, EIICHI NAKANO,  
APPLICANT: MASAKO IZU, ATSUSHI HAYAKAWA, YASUHIKO YOSHIHARA, AND TSUYOSHI  
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER AND NEUSTADT, P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY  
CITY: ARLINGTON  
STATE: VA  
ZIP: 22026  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/852,730  
FILING DATE: 05-07-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-142812  
FILING DATE: 05-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: NORMAN F. OBLON  
REGISTRATION NUMBER: 24,618  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 301 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-852-730-20

Query Match 58.6%; Score 37.5; DB 3; Length 301;  
Best Local Similarity 53.8%; Pred. No. 1.1e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

Qy 1 WY---DPLTKLWL 10  
Db 193 WYSGDDPLNLVWL 205

RESULT 23

```
US-09-328-352-8223
; Sequence 8223, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 8223
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-8223

Query Match          57.8%; Score 37; DB 4; Length 79;
Best Local Similarity 50.0%; Pred. No. 34;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
Db 38 WLSPLTKMKWI 47

RESULT 24
US-09-621-976-6153
; Sequence 6153, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6153
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6153

Query Match          57.8%; Score 37; DB 4; Length 93;
Best Local Similarity 50.0%; Pred. No. 40;
Matches 7; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 1 WYDPLTKLML 10
Db 42 WIDISVPLTKSLMI 55

RESULT 25
US-09-834-759-508
; Sequence 508, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 508
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-759-508

Query Match          57.8%; Score 37; DB 4; Length 158;
Best Local Similarity 62.5%; Pred. No. 69;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9
Db 27 YNPLTNIM 34

RESULT 26
US-09-834-759-507
; Sequence 507, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 507
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-759-507

Query Match          57.8%; Score 37; DB 4; Length 243;
Best Local Similarity 62.5%; Pred. No. 1,1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9
Db 27 YNPLTNIM 34

RESULT 27
US-09-489-039A-8990
; Sequence 8990, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8990
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8990

Query Match          57.8%; Score 37; DB 4; Length 311;
Best Local Similarity 58.3%; Pred. No. 1,4e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
```

Qy 1 WY--DPLTKLWL 10  
|||  
Db 96 WYRNDPRASLWL 107

## RESULT 28

US-09-041-718-3  
; Sequence 3, Application US/09041718A  
; Patent No. 6225075  
; GENERAL INFORMATION:  
; APPLICANT: Bard, Martin  
; TITLE OF INVENTION: DNA encoding steroid methyltransferase  
; FILE REFERENCE: 740,003US1  
; CURRENT FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 383  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-09-041-718-3

Query Match 57.8%; Score 37; DB 3; Length 383;  
Best Local Similarity 66.7%; Pred. No. 1.7e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 9  
|||  
Db 286 WYYPPLTGEM 294

## RESULT 29

US-09-328-352-5102  
; Sequence 5102, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 5102  
; LENGTH: 437  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-5102

Query Match 57.8%; Score 37; DB 4; Length 437;  
Best Local Similarity 44.4%; Pred. No. 1.9e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 9  
|||  
Db 15 WFDPLRSSW 23

## RESULT 30

US-09-976-594-369  
; Sequence 369, Application US/09976594  
; Patent No. 6673549  
; GENERAL INFORMATION:  
; APPLICANT: Furness, Michael  
; APPLICANT: Buchbinder, Jenny  
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LAYER CELL CULTURES TREATED WITH STEROIDS  
; FILE REFERENCE: PA-0041 US  
; CURRENT APPLICATION NUMBER: US/09/976,594  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 60/240,409  
; PRIOR FILING DATE: 2000-10-12

NUMBER OF SEQ ID NOS: 1143  
; SOFTWARE: PERL Program  
; SEQ ID NO 369  
; LENGTH: 819  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; OTHER INFORMATION: Incyte ID No. 6673549 2125081CD1  
US-09-976-594-369

Query Match 57.8%; Score 37; DB 4; Length 819;  
Best Local Similarity 60.0%; Pred. No. 3.6e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10  
|||  
Db 626 WYBPLQKFL 635

## RESULT 31

US-08-680-326-41  
; Sequence 41, Application US/08680326  
; Patent No. 5925733  
; GENERAL INFORMATION:  
; APPLICANT: ROSE, TIMOTHY M.  
; APPLICANT: BOSCH, MARINX  
; APPLICANT: STRAND, KURT  
; APPLICANT: TODARO, GEORGE J.  
; TITLE OF INVENTION: DNA POLYMERASE OF GAMMA HERPES VIRUSES  
; TITLE OF INVENTION: ASSOCIATED WITH KAPOSI'S SARCOMA AND RETROPERITONEAL  
; NUMBER OF SEQUENCES: 152  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/680,326  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schiff, J. Michael  
; REGISTRATION NUMBER: 40,253  
; REFERENCE/DOCKET NUMBER: 29938-20001.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 41:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 985 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-680-326-41

Query Match 57.8%; Score 37; DB 2; Length 985;  
Best Local Similarity 50.0%; Pred. No. 4.3e+02;  
Matches 6; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

Qy 1 WY--DPLTKLWL 10  
|||  
Db 893 WVVVDPLTGIMW 904

RESULT 32  
US-08-164-292B-18  
; Sequence 18, Application US/08164292B  
; Patent No. 5820868  
; GENERAL INFORMATION:  
; APPLICANT: MITTAL, SURESH K.  
; APPLICANT: GRAHAM, FRANK L.  
; APPLICANT: PREVEC, LUDVIG  
; APPLICANT: BABIUK, LORNE A.  
; TITLE OF INVENTION: RECOMBINANT PROTEIN PRODUCTION IN BOVINE  
; TITLE OF INVENTION: ADENOVIRUS EXPRESSION VECTOR SYSTEM  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 345 California Street  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94104-2675  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/164,292B  
; FILING DATE: 09-DEC-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GRACEY, NANCY J.  
; REGISTRATION NUMBER: 28,216  
; REFERENCE/DOCKET NUMBER: 29310-20021.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 677-7000  
; TELEFAX: (415) 677-7522  
; TELEX: 34-0154  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 308 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-164-292B-18

Query Match 56.2%; Score 36; DB 2; Length 308;  
Best Local Similarity 66.7%; Pred. No. 2e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLML 10  
|:|:|:|:|  
Db 71 YNPFTVLML 79

RESULT 33  
US-08-845-623-18  
; Sequence 18, Application US/08845623A  
; Patent No. 6001591  
; GENERAL INFORMATION:  
; APPLICANT: BABIUK, LORNE A.  
; APPLICANT: TIRKOO, SURESH K.  
; APPLICANT: REDDY, POLICE S.  
; TITLE OF INVENTION: BOVINE ADENOVIRUS 3 GENOME  
; FILE REFERENCE: 293102002120  
; CURRENT APPLICATION NUMBER: US/08/845,623A  
; CURRENT FILING DATE: 1997-04-25  
; EARLIER APPLICATION NUMBER: 08/164,294  
; EARLIER FILING DATE: 1993-12-09  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 308  
; TYPE: PRT

ORGANISM: Bovine adenovirus type 3  
US-08-845-623-18

Query Match 56.2%; Score 36; DB 3; Length 308;  
Best Local Similarity 66.7%; Pred. No. 2e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLML 10  
|:|:|:|:|  
Db 71 YNPFTVLML 79

RESULT 34  
US-08-815-927-18  
; Sequence 18, Application US/08815927  
; Patent No. 6086890  
; GENERAL INFORMATION:  
; APPLICANT: MITTAL, SURESH K.  
; APPLICANT: GRAHAM, FRANK L.  
; APPLICANT: PREVEC, LUDVIG  
; APPLICANT: BABIUK, LORNE A.  
; TITLE OF INVENTION: RECOMBINANT PROTEIN PRODUCTION IN BOVINE ADENOVIRUS EXPRESSION  
; TITLE OF INVENTION: VECTOR SYSTEM  
; FILE REFERENCE: 293102002101  
; CURRENT APPLICATION NUMBER: US/08/815,927  
; CURRENT FILING DATE: 1997-03-13  
; EARLIER APPLICATION NUMBER: 08/164,294  
; EARLIER FILING DATE: 1993-12-09  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 308  
; TYPE: PRT  
; ORGANISM: Bovine adenovirus type 3  
; US-08-815-927-18

Query Match 56.2%; Score 36; DB 3; Length 308;  
Best Local Similarity 66.7%; Pred. No. 2e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLML 10  
|:|:|:|:|  
Db 71 YNPFTVLML 79

RESULT 35  
US-09-103-330-18  
; Sequence 18, Application US/09103330A  
; Patent No. 6319716  
; GENERAL INFORMATION:  
; APPLICANT: TIRKOO, SURESH K.  
; APPLICANT: BABIUK, LORNE A.  
; APPLICANT: REDDY, POLICE S.  
; TITLE OF INVENTION: ISOLATION OF MUTANTS IN THE E3 REGION OF THE  
; TITLE OF INVENTION: BOVINE ADENOVIRUS GENOME AND THEIR USE IN VACCINES  
; FILE REFERENCE: 293102002121  
; CURRENT APPLICATION NUMBER: US/09/103,330A  
; CURRENT FILING DATE: 1998-06-23  
; EARLIER APPLICATION NUMBER: 08/880,234  
; EARLIER FILING DATE: 1997-06-23  
; EARLIER APPLICATION NUMBER: 08/164,292  
; EARLIER FILING DATE: 1993-12-09  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 308  
; TYPE: PRT  
; ORGANISM: Bovine adenovirus type 3  
; US-09-103-330-18

Query Match 56.2%; Score 36; DB 4; Length 308;  
Best Local Similarity 66.7%; Pred. No. 2e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKLWL 10  
|:|:|:|  
Db 71 YNPFTVLMWL 79

RESULT 36  
US-09-435-242-18  
; Sequence 18, Application US/09435242  
; Patent No. 6379944  
; GENERAL INFORMATION:  
; APPLICANT: MITTAL, SURESH K.  
; APPLICANT: GRAHAM, FRANK L.  
; APPLICANT: PREVIC, LUDVIG  
; APPLICANT: BABIUK, LORNE A.  
; TITLE OF INVENTION: MAMMALIAN CELL LINES EXPRESSING BOVINE ADENOVIRUS FUNCTIONS  
; FILE REFERENCE: 293102002102  
; CURRENT APPLICATION NUMBER: US/09/435,242  
; CURRENT FILING DATE: 1999-11-05  
; EARLIER APPLICATION NUMBER: 08/815,927  
; EARLIER FILING DATE: 1997-03-13  
; EARLIER APPLICATION NUMBER: 08/164,294  
; EARLIER FILING DATE: 1993-12-09  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.10  
; SEQ ID NO 18  
; LENGTH: 308  
; TYPE: PRT  
; ORGANISM: Bovine adenovirus type 3  
US-09-435-242-18

Query Match 56.2%; Score 36; DB 4; Length 308;  
Best Local Similarity 66.7%; Pred. No. 2e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKLWL 10  
|:|:|:|  
Db 71 YNPFTVLMWL 79

RESULT 37  
US-09-688-019-2  
; Sequence 2, Application US/09688019  
; Patent No. 6566512  
; GENERAL INFORMATION:  
; APPLICANT: Sturley, Stephen L.  
; APPLICANT: Tinkelenberg, Arthur H.  
; TITLE OF INVENTION: ARVI, A PROTEIN INVOLVED IN STEROL UPTAKE AND STEROL HOMEOSTASIS  
; TITLE OF INVENTION: BUDDING YEAST, S. CEREVISIAE, AND A FUNCTIONAL HUMAN ARVI  
; FILE REFERENCE: 0575/58072  
; CURRENT APPLICATION NUMBER: US/09/688,019  
; CURRENT FILING DATE: 2002-04-15  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 321  
; TYPE: PRT  
; ORGANISM: Human  
US-09-688-019-2

Query Match 56.2%; Score 36; DB 4; Length 321;  
Best Local Similarity 66.7%; Pred. No. 2e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKLWL 10  
|:|:|:|  
Db 102 YDRNLRLMWL 110

RESULT 38  
US-09-543-681A-5748  
; Sequence 5748, Application US/09543681A  
; Patent No. 6605709

; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 5748  
; LENGTH: 364  
; TYPE: PRT  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-5748

Query Match 56.2%; Score 36; DB 4; Length 364;  
Best Local Similarity 66.7%; Pred. No. 2.3e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKLWL 10  
|:|:|:|  
Db 200 YDPDKYVWL 208

RESULT 39  
US-09-491-577-36  
; Sequence 36, Application US/09491577  
; Patent No. 6610511  
; GENERAL INFORMATION:  
; APPLICANT: Yale University  
; APPLICANT: Carlson, John R.  
; APPLICANT: Kim, Hunhyong  
; APPLICANT: Clyne, Peter J.  
; APPLICANT: Watt, Coral G.  
; TITLE OF INVENTION: No. 6610511el Family of Odorant Receptor Genes in Drosophila  
; FILE REFERENCE: 44574-5061-US  
; CURRENT APPLICATION NUMBER: US/09/491,577  
; CURRENT FILING DATE: 2000-01-25  
; EARLIER APPLICATION NUMBER: US 60/117,132  
; EARLIER FILING DATE: 1999-01-25  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 36  
; LENGTH: 399  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-491-577-36

Query Match 56.2%; Score 36; DB 4; Length 399;  
Best Local Similarity 50.0%; Pred. No. 2.3e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10  
|:|:|:|  
Db 176 WHDGTLMWV 185

RESULT 40  
US-09-134-000C-4382  
; Sequence 4382, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: PatentIn version 3.1

```
; SEQ ID NO 4382
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4382

Query Match
Best Local Similarity 56.2%; Score 36; DB 4; Length 402;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 3 DPLTKW 9
Db 232 DPLTKW 238

RESULT 41
US-09-107-532A-6726
; Sequence 6726, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENCOM THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Arinello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6726:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 430 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1..430
; SEQUENCE DESCRIPTION: SEQ ID NO: 6726:
US-09-107-532A-6726

Query Match
Best Local Similarity 56.2%; Score 36; DB 4; Length 430;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 3 DPLTKW 9
Db 250 DPLTKW 256
```

```
RESULT 42
US-09-134-000C-5803
; Sequence 5803, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5803
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5803

Query Match
Best Local Similarity 56.2%; Score 36; DB 4; Length 432;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

CY 1 WYDPLTKW 9
Db 297 WYDPLTKW 305

RESULT 43
US-09-914-259-13
; Sequence 13, Application US/0914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 13
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-914-259-13

Query Match
Best Local Similarity 56.2%; Score 36; DB 4; Length 503;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

CY 1 WYDPLTKW 10
Db 258 WYDPLTKW 267

RESULT 44
US-09-543-681A-4359
; Sequence 4359, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
```

PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 8344  
SEQ ID NO 4359  
LENGTH: 641  
TYPE: PRT  
ORGANISM: Proteus mirabilis  
US-09-543-681A-4359

Query Match  
Best Local Similarity 56.2%; Score 36; DB 4; Length 641;  
Pred. No. 4.1e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKML 10  
| | | | |  
Db 253 YKPLDQML 261

RESULT 45  
US-09-328-352-4365  
Sequence 4365, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
FILE REFERENCE: GTC99-03PA  
CURRENT FILING DATE: 1999-06-04  
CURRENT APPLICATION NUMBER: US/09/328,352  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 4365  
LENGTH: 677  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-4365

Query Match  
Best Local Similarity 56.2%; Score 36; DB 4; Length 677;  
Pred. No. 4.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLT 6  
| | | | |  
Db 232 WFDPLT 237

RESULT 46  
US-08-931-952-2  
Sequence 2, Application US/08931952  
Patent No. 6054569  
GENERAL INFORMATION:  
APPLICANT: Bennett, Clark  
APPLICANT: Laliberte, Maryse  
APPLICANT: Gu, Kangfu  
APPLICANT: Zimmerman, Joseph  
APPLICANT: Tkalec, Lydia  
APPLICANT: Danagher, Pamela  
APPLICANT: Fink, Dominique  
APPLICANT: Linhardt, Robert  
TITLE OF INVENTION: CHONDROITIN LYASE ENZYMES  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: 1100 Peachtree Street, Suite 2800  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309-4530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/931,952

FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/272,247  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: IT103  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 815-6508  
TELEFAX: (404) 815-6555  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 700 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..23  
OTHER INFORMATION: /note= "Amino acids 1 through 23  
OTHER INFORMATION: are a leader peptide."  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..700  
OTHER INFORMATION: /note= "Amino acid sequence  
OTHER INFORMATION: of chondroitinase AC from Flavobacterium  
OTHER INFORMATION: heparinum."  
US-08-931-952-2

Query Match  
Best Local Similarity 56.2%; Score 36; DB 3; Length 700;  
Pred. No. 4.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PLTKLM 9  
| | | | |  
Db 422 PLTKLM 427

RESULT 47  
US-08-272-247-2  
Sequence 2, Application US/08272247  
Patent No. 6093563  
GENERAL INFORMATION:  
APPLICANT: Bennett, Clark  
APPLICANT: Laliberte, Maryse  
APPLICANT: Gu, Kangfu  
APPLICANT: Zimmerman, Joseph  
APPLICANT: Tkalec, Lydia  
APPLICANT: Danagher, Pamela  
APPLICANT: Fink, Dominique  
APPLICANT: Linhardt, Robert  
TITLE OF INVENTION: CHONDROITIN LYASE ENZYMES  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: 1100 Peachtree Street, Suite 2800  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309-4530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/272,247  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.

REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: IT103  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 815-6508  
TELEFAX: (404) 815-6555  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 700 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..23 /note="Amino acids 1 through 23  
OTHER INFORMATION: are a leader peptide."  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..700  
OTHER INFORMATION: /note="Amino acid sequence  
of chondroitinase AC from Flavobacterium  
heparinum."  
US-08-272-247-2  
Query Match 56.2% Score 36; DB 3; Length 700;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 PLTKLM 9  
DB 422 PLTKLM 427  
RESULT 48  
PCT-US95-08560-2  
Sequence 2, Application PC/TUS9508560  
GENERAL INFORMATION:  
APPLICANT: IREX TECHNOLOGIES R AND D, INC.  
TITLE OF INVENTION: CHONDROITIN LYASE ENZYMES  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: 2800 One Atlantic Center, 1201 West Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/08560  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/272,247  
FILING DATE: 08-Jun-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: IT103PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 873-8794  
TELEFAX: (404) 873-8795  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 700 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..23 /note="Amino acids 1 through 23 are a leader  
OTHER INFORMATION: peptide."  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..700  
OTHER INFORMATION: /note="Amino acid sequence  
of chondroitinase AC from Flavobacterium  
heparinum."  
PCT-US95-08560-2

Query Match 56.2% Score 36; DB 5; Length 700;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PLTKLM 9  
DB 422 PLTKLM 427

RESULT 49  
US-09-540-236-3595  
Sequence 3595, Application US/09540236  
Patent No. 6673910  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS  
FILE REFERENCE: 2709.2005-001  
CURRENT APPLICATION NUMBER: US/09/540.236  
CURRENT FILING DATE: 2000-04-04  
NUMBER OF SEQ ID NOS: 3840  
SEQ ID NO 3595  
LENGTH: 713  
TYPE: PRT  
ORGANISM: M.catarrhalis  
US-09-540-236-3595

Query Match 56.2% Score 36; DB 4; Length 713;  
Best Local Similarity 83.3%; Pred. No. 4.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLT 6  
DB 271 WYDPLT 276

RESULT 50  
US-09-688-188B-91  
Sequence 91, Application US/09688188B  
Patent No. 6656716  
GENERAL INFORMATION:  
APPLICANT: PLOWMAN, GREGORY  
APPLICANT: MARTINEZ, RICARDO  
APPLICANT: MYHRE, DAVID  
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
FILE REFERENCE: 038602/0328  
CURRENT APPLICATION NUMBER: US/09/688.188B  
CURRENT FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: 09/291,417  
PRIOR FILING DATE: 1999-04-14  
PRIOR APPLICATION NUMBER: 60/081,764  
PRIOR FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 155  
SOFTWARE: Patent Ver. 2.1  
SEQ ID NO 91  
LENGTH: 842  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-688-188B-91



Query Match 56.2%; Score 36; DB 4; Length 842;  
Best Local Similarity 50.0%; Pred. No. 5.4e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10  
||:|:|  
Db 647 WYEPWQKFWL 656

RESULT 51  
US-09-291-417D-91  
; Sequence 91, Application US/09291417D  
; Patent No. 6680170  
; GENERAL INFORMATION:  
; APPLICANT: PLOWMAN, GREGORY  
; APPLICANT: MARTINEZ, RICARDO  
; APPLICANT: WHITE, DAVID  
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
; FILE REFERENCE: 038602/0329  
; CURRENT APPLICATION NUMBER: US/09/291,417D  
; PRIOR FILING DATE: 1999-04-13  
; PRIOR APPLICATION NUMBER: 60/081,784  
; NUMBER OF SEQ ID NOS: 155  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 91  
; LENGTH: 842  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-291-417D-91

Query Match 56.2%; Score 36; DB 4; Length 842;  
Best Local Similarity 50.0%; Pred. No. 5.4e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 WYDPLTKLML 10  
||:|:|  
Db 647 WYEPWQKFWL 656

RESULT 52  
US-09-543-681A-8019  
; Sequence 8019, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; PRIOR FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 8019  
; LENGTH: 1129  
; TYPE: PRT  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-8019

Query Match 56.2%; Score 36; DB 4; Length 1129;  
Best Local Similarity 62.5%; Pred. No. 7.2e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 WYDPLTKL 8  
||:|:|  
Db 36 WYDPIINPL 43

RESULT 53  
US-08-052-681-1  
; Sequence 1, Application US/08052681  
; Patent No. 5314819

GENERAL INFORMATION:  
\* APPLICANT: Kazunori YAMADA et al  
; TITLE OF INVENTION: NOVEL PROTEIN HAVING NITRILE HYDRATASE  
; TITLE OF INVENTION: ACTIVITY AND THE GENE ENCODING THE SAME, AND A METHOD FOR PRODUCING THE SAME  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESSES:  
; ADDRESS: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/052,681  
; FILING DATE: 19930427  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 198 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM:  
; STRAIN: Rhizobium sp. MC12643  
; INDIVIDUAL ISOLATE:  
; DEVELOPMENTAL STAGE:  
; HAPLOTYPE:  
; TISSUE TYPE:  
; CELL TYPE:  
; ORGANELLER:  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE:  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT:  
; MAP POSITION:  
; UNITS:  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
; PUBLICATION INFORMATION:  
; AUTHORS:  
; TITLE:  
; JOURNAL:  
; VOLUME:  
; ISSUE:  
; PAGES:  
; DATE:

DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-052-681-1

Query Match 54.7%; Score 35; DB 1; Length 198;  
Best Local Similarity 60.0%; Pred. No. 1.8e+02;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WYDPLTKML 10  
Db 57 WTDPEFKKWL 66

RESULT 54  
US-09-252-991A-20618  
Sequence 20618, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 20618  
LENGTH: 220  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-20618

Query Match 54.7%; Score 35; DB 4; Length 220;  
Best Local Similarity 44.4%; Pred. No. 2e+02;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKML 9  
Db 11 WMSPTKRW 19

RESULT 55  
US-09-150-133-11  
Sequence 11, Application US/09150133B  
Patent No. 6060295  
GENERAL INFORMATION:  
APPLICANT: The Board of Regents of the University of Oklahoma  
TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERASES, NUCLEIC ACIDS ENCODING  
FILE REFERENCE: 5820.504  
CURRENT APPLICATION NUMBER: US/09/150,133B  
CURRENT FILING DATE: 1998-09-09  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: Wordperfect 5.1 (saved in ASCII format)  
SEQ ID NO 11  
LENGTH: 359  
TYPE: PRT  
ORGANISM: Caenorhabditis elegans  
US-09-150-133-11

Query Match 54.7%; Score 35; DB 3; Length 359;  
Best Local Similarity 75.0%; Pred. No. 3.3e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DPLTKML 10  
Db 171 DPTALML 178

RESULT 56  
US-09-150-141-11  
Sequence 11, Application US/09150141B  
Patent No. 6071732  
GENERAL INFORMATION:  
APPLICANT: The Board of Regents of the University of Oklahoma  
TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERASES, NUCLEIC ACIDS ENCODING  
FILE REFERENCE: 5820.495  
CURRENT APPLICATION NUMBER: US/09/150,141B  
CURRENT FILING DATE: 1998-09-09  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: Wordperfect 5.1 (saved in ASCII format)  
SEQ ID NO 11  
LENGTH: 359  
TYPE: PRT  
ORGANISM: Caenorhabditis elegans  
US-09-150-141-11

Query Match 54.7%; Score 35; DB 3; Length 359;  
Best Local Similarity 75.0%; Pred. No. 3.3e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DPLTKML 10  
Db 171 DPTALML 178

RESULT 57  
US-09-374-493-11  
Sequence 11, Application US/09374493  
Patent No. 6204016  
GENERAL INFORMATION:  
APPLICANT: The Board of Regents of the University of Oklahoma  
TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERASES AND METHODS OF USE THEREOF  
FILE REFERENCE: 5820.546  
CURRENT APPLICATION NUMBER: US/09/374,493  
CURRENT FILING DATE: 1999-08-13  
EARLIER APPLICATION NUMBER: 09/150,133  
EARLIER FILING DATE: 1998-09-09  
EARLIER APPLICATION NUMBER: 60/072,994  
EARLIER FILING DATE: 1998-01-29  
EARLIER APPLICATION NUMBER: PCT/US99/16750  
EARLIER FILING DATE: 1999-07-23  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: Wordperfect 8.0 (saved in ASCII format)  
SEQ ID NO 11  
LENGTH: 359  
TYPE: PRT  
ORGANISM: Caenorhabditis elegans  
US-09-374-493-11

Query Match 54.7%; Score 35; DB 3; Length 359;  
Best Local Similarity 75.0%; Pred. No. 3.3e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DPLTKML 10  
Db 171 DPTALML 178

RESULT 58  
US-09-374-824-11  
Sequence 11, Application US/09374824  
Patent No. 6207414  
GENERAL INFORMATION:  
APPLICANT: The Board of Regents of the University of Oklahoma  
TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERASES AND METHODS OF USE THEREOF  
FILE REFERENCE: 5820.547  
CURRENT APPLICATION NUMBER: US/09/374,824  
CURRENT FILING DATE: 1999-08-13  
EARLIER APPLICATION NUMBER: 09/150,133

```
; EARLIER FILING DATE: 1998-09-09
; EARLIER APPLICATION NUMBER: 60/072,994
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: PCT/US99/16750
; EARLIER FILING DATE: 1999-07-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Wordperfect 8.0 (saved in ASCII format)
; SEQ ID NO 11
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-374-824-11

Query Match
Best Local Similarity 54.7%; Score 35; DB 3; Length 359;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DPLTKLWL 10
Db 171 DPTALWL 178

RESULT 59
US-09-374-492-11
; Sequence 11, Application US/09374492
; Patent No. 6207432
; GENERAL INFORMATION:
; APPLICANT: The Board of Regents of the University of Oklahoma
; TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERASES AND METHODS OF USE THEREOF
; FILE REFERENCE: 5820.545
; CURRENT FILING DATE: 1999-08-13
; EARLIER APPLICATION NUMBER: 09/150,141
; EARLIER FILING DATE: 1998-09-09
; EARLIER APPLICATION NUMBER: 60/072,994
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: PCT/US99/16750
; EARLIER FILING DATE: 1999-07-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Wordperfect 8.0 (saved in ASCII format)
; SEQ ID NO 11
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-374-492-11

Query Match
Best Local Similarity 54.7%; Score 35; DB 3; Length 359;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DPLTKLWL 10
Db 171 DPTALWL 178

RESULT 60
US-09-785-343-11
; Sequence 11, Application US/09785343
; Patent No. 6605455
; GENERAL INFORMATION:
; APPLICANT: The Board of Regents of the University of Oklahoma
; TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERASES AND METHODS OF USE THEREOF
; FILE REFERENCE: 5827.003
; CURRENT FILING DATE: 2001-02-16
; EARLIER APPLICATION NUMBER: 09/150,133
; EARLIER FILING DATE: 1998-09-09
; EARLIER APPLICATION NUMBER: 60/072,994
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: PCT/US99/16750
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Wordperfect 8.0 (saved in ASCII format)
```

```
; SEQ ID NO 11
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-785-343-11

Query Match
Best Local Similarity 54.7%; Score 35; DB 4; Length 359;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DPLTKLWL 10
Db 171 DPTALWL 178

RESULT 61
US-09-724-566A-75
; Sequence 75, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEWC2
; CURRENT FILING DATE: 2000-11-28
; EARLIER APPLICATION NUMBER: US/09/724,566A
; EARLIER FILING DATE: 2000-02-10
; EARLIER APPLICATION NUMBER: US 09/501,708
; EARLIER FILING DATE: 2000-02-10
; EARLIER APPLICATION NUMBER: 60/119,571
; EARLIER FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 60/139,172
; EARLIER FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PastsEQ for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-566A-75

Query Match
Best Local Similarity 54.7%; Score 35; DB 4; Length 361;
Best Local Similarity 44.4%; Pred. No. 3.3e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
Db 188 WYPIRREW 196

RESULT 62
US-09-724-566A-71
; Sequence 71, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
```

```
APPLICANT: Wang, Shuwen
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
FILE REFERENCE: 228-US-NEWC2
CURRENT APPLICATION NUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/501,708
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/139,172
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 71
LENGTH: 374
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-566A-71
```

```
Query Match          54.7%; Score 35; DB 4; Length 374;
Best Local Similarity 44.4%; Pred. No. 3.6e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 WYDPLTKLW 9
Db      205 WYTPIRREW 213
```

```
RESULT 63
US-09-724-566A-70
Sequence 70, Application US/09724566A
Patent No. 6627739
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Basl, Guribajal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: John, Varghese
APPLICANT: Power, Michael
APPLICANT: Sinha, Sukanto
APPLICANT: Tatsuno, Gwen
APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Methods
FILE REFERENCE: 228-US-NEWC2
CURRENT APPLICATION NUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/501,708
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/139,172
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 70
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-566A-70
```

```
Query Match          54.7%; Score 35; DB 4; Length 390;
Best Local Similarity 44.4%; Pred. No. 3.6e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 WYDPLTKLW 9
Db      188 WYTPIRREW 196
```

```
RESULT 64
US-09-724-566A-68
Sequence 68, Application US/09724566A
Patent No. 6627739
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Basl, Guribajal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: John, Varghese
APPLICANT: Power, Michael
APPLICANT: Sinha, Sukanto
APPLICANT: Tatsuno, Gwen
APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Methods
FILE REFERENCE: 228-US-NEWC2
CURRENT APPLICATION NUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/501,708
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/139,172
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 68
LENGTH: 395
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-566A-68
```

```
Query Match          54.7%; Score 35; DB 4; Length 395;
Best Local Similarity 44.4%; Pred. No. 3.6e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 WYDPLTKLW 9
Db      193 WYTPIRREW 201
```

```
RESULT 65
US-09-724-566A-58
Sequence 58, Application US/09724566A
Patent No. 6627739
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Basl, Guribajal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: John, Varghese
APPLICANT: Power, Michael
APPLICANT: Sinha, Sukanto
APPLICANT: Tatsuno, Gwen
APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Methods
FILE REFERENCE: 228-US-NEWC2
CURRENT APPLICATION NUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/501,708
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/139,172
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
```

SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 58  
; LENGTH: 407  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-724-566A-58

Query Match 54.7%; Score 35; DB 4; Length 407;  
Best Local Similarity 44.4%; Pred. No. 3.9e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 WYDPLTKLM 9  
|||:|  
Db 205 WYTPIRREM 213

RESULT 66  
US-09-724-566A-57  
; Sequence 57, Application US/09724566A  
; Patent No. 6627739  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, John P.  
; APPLICANT: Basi, Gurigbal  
; APPLICANT: Doane, Minh Tam  
; APPLICANT: Frigon, No. 6627739mand  
; APPLICANT: John, Varghese  
; APPLICANT: Power, Michael  
; APPLICANT: Sinha, Sukanto  
; APPLICANT: Tatsuno, Gwen  
; APPLICANT: Tung, Jay  
; APPLICANT: Wang, Shuwen

; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and  
; FILE REFERENCE: 228-US-NEWC2  
; CURRENT APPLICATION NUMBER: US/09/724,566A  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 09/501,708  
; PRIOR FILING DATE: 2000-02-10  
; PRIOR APPLICATION NUMBER: 60/119,571  
; PRIOR FILING DATE: 1999-02-10  
; PRIOR APPLICATION NUMBER: 60/139,172  
; PRIOR FILING DATE: 1999-06-15  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 57  
; LENGTH: 419  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-724-566A-57

Query Match 54.7%; Score 35; DB 4; Length 419;  
Best Local Similarity 44.4%; Pred. No. 3.9e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 WYDPLTKLM 9  
|||:|  
Db 250 WYTPIRREM 258

RESULT 67  
US-09-724-566A-60  
; Sequence 60, Application US/09724566A  
; Patent No. 6627739  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, John P.  
; APPLICANT: Basi, Gurigbal  
; APPLICANT: Doane, Minh Tam  
; APPLICANT: Frigon, No. 6627739mand  
; APPLICANT: John, Varghese  
; APPLICANT: Power, Michael  
; APPLICANT: Sinha, Sukanto  
; APPLICANT: Tatsuno, Gwen

; APPLICANT: Tung, Jay  
; APPLICANT: Wang, Shuwen  
; APPLICANT: McConlogue, Lisa  
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and  
; FILE REFERENCE: 228-US-NEWC2  
; CURRENT APPLICATION NUMBER: US/09/724,566A  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 09/501,708  
; PRIOR FILING DATE: 2000-02-10  
; PRIOR APPLICATION NUMBER: 60/119,571  
; PRIOR FILING DATE: 1999-02-10  
; PRIOR APPLICATION NUMBER: 60/139,172  
; PRIOR FILING DATE: 1999-06-15  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 60  
; LENGTH: 420  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-724-566A-60

Query Match 54.7%; Score 35; DB 4; Length 420;  
Best Local Similarity 44.4%; Pred. No. 3.9e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 WYDPLTKLM 9  
|||:|  
Db 250 WYTPIRREM 258

RESULT 68  
US-08-879-337-5  
; Sequence 5, Application US/08879337B  
; Patent No. 6639130  
; GENERAL INFORMATION:  
; APPLICANT: Jang, Jyan-Chyun  
; APPLICANT: Sheen, Jen  
; TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF  
; FILE REFERENCE: 00786/338001  
; CURRENT APPLICATION NUMBER: US/08/879,337B  
; CURRENT FILING DATE: 1997-06-20  
; EARLIER APPLICATION NUMBER: 60/022,086  
; EARLIER FILING DATE: 1996-06-21  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 424  
; TYPE: PRT  
; ORGANISM: Schizosaccharomyces pombe  
US-08-879-337-5

Query Match 54.7%; Score 35; DB 4; Length 424;  
Best Local Similarity 55.6%; Pred. No. 3.9e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 WYDPLTKLM 9  
|||:|  
Db 72 WFTLTLML 80

RESULT 69  
US-09-548-372D-28  
; Sequence 28, Application US/09548372D  
; Patent No. 6420534  
; GENERAL INFORMATION:  
; APPLICANT: GURNEY ET AL.  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES  
; FILE REFERENCE: 29915/62801  
; CURRENT APPLICATION NUMBER: US/09/548,372D  
; CURRENT FILING DATE: 2000-04-12  
; PRIOR APPLICATION NUMBER: US 60/155,493

```

; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-28
```

```

Query Match          54.7%; Score 35; DB 4; Length 425;
Best Local Similarity 44.4%; Pred. No. 3.9e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 WYDPLTKLM 9
|||:|
Db      222 WYPIRREW 230
```

```

RESULT 70
US-09-548-367D-28
; Sequence 28, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-28
```

```

Query Match          54.7%; Score 35; DB 4; Length 425;
Best Local Similarity 44.4%; Pred. No. 3.9e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 WYDPLTKLM 9
|||:|
Db      222 WYPIRREW 230
```

```

RESULT 71
US-09-551-853D-28
; Sequence 28, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
```

```

; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-853D-28
```

```

Query Match          54.7%; Score 35; DB 4; Length 425;
Best Local Similarity 44.4%; Pred. No. 3.9e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 WYDPLTKLM 9
|||:|
Db      222 WYPIRREW 230
```

```

RESULT 72
US-09-548-372D-51
; Sequence 51, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Aep2 (b) delta TM
US-09-548-372D-51
```

```

Query Match          54.7%; Score 35; DB 4; Length 428;
Best Local Similarity 44.4%; Pred. No. 4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 WYDPLTKLM 9
|||:|
Db      225 WYPIRREW 233
```

```

RESULT 73
US-09-548-367D-51
; Sequence 51, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
```

PRIOR FILING DATE: 1999-09-23  
PRIOR APPLICATION NUMBER: US 09/404,133  
PRIOR FILING DATE: 1999-09-23  
PRIOR APPLICATION NUMBER: PCT/US99/20881  
PRIOR FILING DATE: 1999-09-23  
PRIOR APPLICATION NUMBER: US 60/101,594  
PRIOR FILING DATE: 1998-09-24  
NUMBER OF SEQ ID NOS: 73  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 51  
LENGTH: 428  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Hu-Asp2 (b) delta TM  
US-09-548-367D-51

Query Match 54.7%; Score 35; DB 4; Length 428;  
Best Local Similarity 44.4%; Pred. No. 4e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9  
Db 225 WYTPIRREW 233

RESULT 74  
US-09-551-853D-51  
Sequence 51, Application US/09551853D  
Patent No. 6500667  
GENERAL INFORMATION:  
APPLICANT: GURNEY ET AL.  
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES  
FILE REFERENCE: 29915/6280L  
CURRENT FILING DATE: 2000-04-18  
PRIOR APPLICATION NUMBER: US 60/155,493  
PRIOR FILING DATE: 1999-09-23  
PRIOR APPLICATION NUMBER: US 09/404,133  
PRIOR FILING DATE: 1999-09-23  
PRIOR APPLICATION NUMBER: PCT/US99/20881  
PRIOR FILING DATE: 1999-09-23  
PRIOR APPLICATION NUMBER: US 60/101,594  
PRIOR FILING DATE: 1998-09-24  
NUMBER OF SEQ ID NOS: 73  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 51  
LENGTH: 428  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Hu-Asp2 (b) delta TM  
US-09-551-853D-51

Query Match 54.7%; Score 35; DB 4; Length 428;  
Best Local Similarity 44.4%; Pred. No. 4e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9  
Db 225 WYTPIRREW 233

RESULT 75  
US-09-724-566A-74  
Sequence 74, Application US/09724566A  
Patent No. 6627739  
GENERAL INFORMATION:  
APPLICANT: Anderson, John P.  
APPLICANT: Baal, Gurigbal  
APPLICANT: Doane, Minh Tam  
APPLICANT: Frigon, No. 6627739mand

APPLICANT: John, Varghese  
APPLICANT: Power, Michael  
APPLICANT: Sinha, Sukanto  
APPLICANT: Tatsuno, Gwen  
APPLICANT: Tung, Jay  
APPLICANT: Wang, Shuwen  
APPLICANT: McConlogue, Lisa  
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and  
FILE REFERENCE: 228-US-NEWC2  
CURRENT FILING DATE: US/09/724,566A  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: US 09/501,708  
PRIOR FILING DATE: 2000-02-10  
PRIOR APPLICATION NUMBER: 60/119,571  
PRIOR FILING DATE: 1999-02-10  
PRIOR APPLICATION NUMBER: 60/139,172  
PRIOR FILING DATE: 1999-06-15  
NUMBER OF SEQ ID NOS: 104  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 74  
LENGTH: 431  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-566A-74

Query Match 54.7%; Score 35; DB 4; Length 431;  
Best Local Similarity 44.4%; Pred. No. 4e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9  
Db 229 WYTPIRREW 237

RESULT 76  
US-09-548-372D-26  
Sequence 26, Application US/09548372D  
Patent No. 6420534  
GENERAL INFORMATION:  
APPLICANT: GURNEY ET AL.  
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES  
FILE REFERENCE: 29915/6280L  
CURRENT FILING DATE: US/09/548,372D  
PRIOR FILING DATE: 2000-04-12  
PRIOR APPLICATION NUMBER: US 60/155,493  
PRIOR FILING DATE: 1999-09-23  
PRIOR APPLICATION NUMBER: US 09/404,133  
PRIOR FILING DATE: 1999-09-23  
PRIOR APPLICATION NUMBER: PCT/US99/20881  
PRIOR FILING DATE: 1999-09-23  
PRIOR APPLICATION NUMBER: US 60/101,594  
PRIOR FILING DATE: 1998-09-24  
NUMBER OF SEQ ID NOS: 73  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 26  
LENGTH: 433  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-548-372D-26

Query Match 54.7%; Score 35; DB 4; Length 433;  
Best Local Similarity 44.4%; Pred. No. 4e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9  
Db 230 WYTPIRREW 238

RESULT 77  
US-09-548-367D-26

```
; Sequence 26, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 26
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-26
```

```
Query Match          54.7%; Score 35; DB 4; Length 433;
Best Local Similarity 44.4%; Pred. No. 4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 WYDPLTKLM 9
Db      230 WYTPIRREW 238
```

```
RESULT 78
US-09-551-853D-26
; Sequence 26, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 26
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-853D-26
```

```
Query Match          54.7%; Score 35; DB 4; Length 433;
Best Local Similarity 44.4%; Pred. No. 4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 WYDPLTKLM 9
Db      230 WYTPIRREW 238
```

```
RESULT 79
US-09-548-372D-53
; Sequence 53, Application US/09548372D
```

```
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 53
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-372D-53
```

```
Query Match          54.7%; Score 35; DB 4; Length 434;
Best Local Similarity 44.4%; Pred. No. 4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 WYDPLTKLM 9
Db      225 WYTPIRREW 233
```

```
RESULT 80
US-09-548-367D-53
; Sequence 53, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 53
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-367D-53
```

```
Query Match          54.7%; Score 35; DB 4; Length 434;
Best Local Similarity 44.4%; Pred. No. 4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 WYDPLTKLM 9
Db      225 WYTPIRREW 233
```



```
RESULT 81
US-09-551-853D-53
; Sequence 53, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hu-Asp2 (D) delta TM
US-09-551-853D-53

Query Match          54.7%; Score 35; DB 4; Length 434;
Best Local Similarity 44.4%; Pred. No. 4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLM 9
Db 225 WYTPIRREW 233

RESULT 82
US-09-724-566A-69
; Sequence 69, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Baal, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-566A-69
```

```
Query Match          54.7%; Score 35; DB 4; Length 439;
Best Local Similarity 44.4%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLM 9
Db 188 WYTPIRREW 196

RESULT 83
US-09-724-566A-67
; Sequence 67, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Baal, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-566A-67

Query Match          54.7%; Score 35; DB 4; Length 444;
Best Local Similarity 44.4%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLM 9
Db 193 WYTPIRREW 201

RESULT 84
US-09-548-372D-22
; Sequence 22, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
```

```
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 22
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-22
```

```
Query Match          54.7%; Score 35; DB 4; Length 446;
Best Local Similarity 44.4%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 WYDPLTKLM 9
        |||:|
Db      243 WYTPIRREM 251
```

```
RESULT 85
US-09-548-367D-22
; Sequence 22, Application US/09548367D
; Patent No. 6440698
```

```
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 22
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-22
```

```
Query Match          54.7%; Score 35; DB 4; Length 446;
Best Local Similarity 44.4%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 WYDPLTKLM 9
        |||:|
Db      243 WYTPIRREM 251
```

```
RESULT 86
US-09-551-853D-22
; Sequence 22, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
```

```
; SEQ ID NO 22
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-853D-22
```

```
Query Match          54.7%; Score 35; DB 4; Length 446;
Best Local Similarity 44.4%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 WYDPLTKLM 9
        |||:|
Db      243 WYTPIRREM 251
```

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RESULT 87
US-09-230-371A-28
; Sequence 28, Application US/09230371A
; Patent No. 6348586
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bonenzky, Roy A
; APPLICANT: Russo, James J
; APPLICANT: Edelman, Isidore S
; APPLICANT: Moore, Patrick S
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
; FILE REFERENCE: 45185-G-PCT-US
; CURRENT APPLICATION NUMBER: US/09/230,371A
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US97/13346
; PRIOR FILING DATE: 1997-07-22
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 28
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-230-371A-28
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Query Match          54.7%; Score 35; DB 4; Length 449;
Best Local Similarity 85.7%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      4 PLTKLML 10
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Db      398 PLVRLWL 404
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RESULT 88
US-09-724-566A-59
; Sequence 59, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Suktano
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEMC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
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;; PRIOR FILING DATE: 1999-02-10  
;; PRIOR APPLICATION NUMBER: 60/139,172  
;; PRIOR FILING DATE: 1999-06-15  
;; NUMBER OF SEQ ID NOS: 104  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 59  
;; LENGTH: 452  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-724-566A-59

Query Match 54.7%; Score 35; DB 4; Length 453;  
Best Local Similarity 44.4%; Pred. No. 4.2e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9  
|||:|  
Db 250 WYTPIRREW 258

RESULT 89  
US-09-548-372D-30  
; Sequence 30, Application US/09548372D  
; Patent No. 6420534  
; GENERAL INFORMATION:  
; APPLICANT: GURNEY ET AL.  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES  
; FILE REFERENCE: 29915/62801  
; CURRENT FILING DATE: 2000-04-12  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: US 60/155,493  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: US 09/404,133  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: PCT/US99/20881  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: US 60/101,594  
; PRIOR FILING DATE: 1998-09-24  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 30  
; LENGTH: 453  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-548-372D-30

Query Match 54.7%; Score 35; DB 4; Length 453;  
Best Local Similarity 44.4%; Pred. No. 4.2e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9  
|||:|  
Db 250 WYTPIRREW 258

RESULT 90  
US-09-548-367D-30  
; Sequence 30, Application US/09548367D  
; Patent No. 6440698  
; GENERAL INFORMATION:  
; APPLICANT: GURNEY ET AL.  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES  
; FILE REFERENCE: 29915/62808  
; CURRENT FILING DATE: 2000-04-12  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: US 60/155,493  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: US 09/404,133  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: PCT/US99/20881  
; PRIOR FILING DATE: 1999-09-23

;; PRIOR APPLICATION NUMBER: US 60/101,594  
;; PRIOR FILING DATE: 1998-09-24  
;; NUMBER OF SEQ ID NOS: 73  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 30  
;; LENGTH: 453  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-548-367D-30

Query Match 54.7%; Score 35; DB 4; Length 453;  
Best Local Similarity 44.4%; Pred. No. 4.2e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9  
|||:|  
Db 250 WYTPIRREW 258

RESULT 91  
US-09-551-853D-30  
; Sequence 30, Application US/09551853D  
; Patent No. 6500667  
; GENERAL INFORMATION:  
; APPLICANT: GURNEY ET AL.  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES  
; FILE REFERENCE: 29915/62801  
; CURRENT FILING DATE: 2000-04-18  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: US 60/155,493  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: US 09/404,133  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: PCT/US99/20881  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: US 60/101,594  
; PRIOR FILING DATE: 1998-09-24  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 30  
; LENGTH: 453  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-551-853D-30

Query Match 54.7%; Score 35; DB 4; Length 453;  
Best Local Similarity 44.4%; Pred. No. 4.2e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9  
|||:|  
Db 250 WYTPIRREW 258

RESULT 92  
US-09-724-566A-43  
; Sequence 43, Application US/09724566A  
; Patent No. 6627739  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, John P.  
; APPLICANT: Basi, Guribdal  
; APPLICANT: Doane, Minh Tam  
; APPLICANT: Frigon, No. 6627739mand  
; APPLICANT: John, Varghese  
; APPLICANT: Power, Michael  
; APPLICANT: Sinha, Sukanto  
; APPLICANT: Tatsuno, Gwen  
; APPLICANT: Tung, Jay  
; APPLICANT: Wang, Shuwen  
; APPLICANT: McConlogue, Lisa  
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and Methods

FILE REFERENCE: 228-US-NEWC2  
 CURRENT APPLICATION NUMBER: US/09/724,566A  
 CURRENT FILING DATE: 2000-11-28  
 PRIOR APPLICATION NUMBER: US 09/501,708  
 PRIOR FILING DATE: 2000-02-10  
 PRIOR APPLICATION NUMBER: 60/119,571  
 PRIOR FILING DATE: 1999-02-10  
 PRIOR APPLICATION NUMBER: 60/139,172  
 PRIOR FILING DATE: 1999-06-15  
 NUMBER OF SEQ ID NOS: 104  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 43  
 LENGTH: 456  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-724-566A-43

Query Match 54.7%; Score 35; DB 4; Length 456;  
 Best Local Similarity 44.4%; Pred. No. 4.2e+02;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLM 9  
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 Db 205 WYTPIRREW 213

RESULT 93  
 US-09-548-372D-24  
 Sequence 24, Application US/09548372D  
 Patent No. 6420534  
 GENERAL INFORMATION:  
 APPLICANT: GURNEY ET AL.  
 TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES  
 FILE REFERENCE: 29915/62801  
 CURRENT APPLICATION NUMBER: US/09/548,372D  
 CURRENT FILING DATE: 2000-04-12  
 PRIOR APPLICATION NUMBER: US 60/155,493  
 PRIOR FILING DATE: 1999-09-23  
 PRIOR APPLICATION NUMBER: US 09/404,133  
 PRIOR FILING DATE: 1999-09-23  
 PRIOR APPLICATION NUMBER: PCT/US99/20881  
 PRIOR FILING DATE: 1999-09-23  
 PRIOR APPLICATION NUMBER: US 60/101,594  
 PRIOR FILING DATE: 1998-09-24  
 NUMBER OF SEQ ID NOS: 73  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 24  
 LENGTH: 459  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-548-372D-24

Query Match 54.7%; Score 35; DB 4; Length 459;  
 Best Local Similarity 44.4%; Pred. No. 4.2e+02;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLM 9  
 |||:|  
 Db 256 WYTPIRREW 264

RESULT 94  
 US-09-548-372D-32  
 Sequence 32, Application US/09548372D  
 Patent No. 6420534  
 GENERAL INFORMATION:  
 APPLICANT: GURNEY ET AL.  
 TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES  
 FILE REFERENCE: 29915/62801  
 CURRENT APPLICATION NUMBER: US/09/548,372D  
 CURRENT FILING DATE: 2000-04-12

PRIOR APPLICATION NUMBER: US 60/155,493  
 PRIOR FILING DATE: 1999-09-23  
 PRIOR APPLICATION NUMBER: US 09/404,133  
 PRIOR FILING DATE: 1999-09-23  
 PRIOR APPLICATION NUMBER: PCT/US99/20881  
 PRIOR FILING DATE: 1999-09-23  
 PRIOR APPLICATION NUMBER: US 60/101,594  
 PRIOR FILING DATE: 1998-09-24  
 NUMBER OF SEQ ID NOS: 73  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 32  
 LENGTH: 459  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-548-372D-32

Query Match 54.7%; Score 35; DB 4; Length 459;  
 Best Local Similarity 44.4%; Pred. No. 4.2e+02;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLM 9  
 |||:|  
 Db 250 WYTPIRREW 258

RESULT 95  
 US-09-548-367D-24  
 Sequence 24, Application US/09548367D  
 Patent No. 6440698  
 GENERAL INFORMATION:  
 APPLICANT: GURNEY ET AL.  
 TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES  
 FILE REFERENCE: 29915/62801  
 CURRENT APPLICATION NUMBER: US/09/548,367D  
 CURRENT FILING DATE: 2000-04-12  
 PRIOR APPLICATION NUMBER: US 60/155,493  
 PRIOR FILING DATE: 1999-09-23  
 PRIOR APPLICATION NUMBER: US 09/404,133  
 PRIOR FILING DATE: 1999-09-23  
 PRIOR APPLICATION NUMBER: PCT/US99/20881  
 PRIOR FILING DATE: 1999-09-23  
 PRIOR APPLICATION NUMBER: US 60/101,594  
 PRIOR FILING DATE: 1998-09-24  
 NUMBER OF SEQ ID NOS: 73  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 24  
 LENGTH: 459  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-548-367D-24

Query Match 54.7%; Score 35; DB 4; Length 459;  
 Best Local Similarity 44.4%; Pred. No. 4.2e+02;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLM 9  
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 Db 256 WYTPIRREW 264

RESULT 96  
 US-09-548-367D-32  
 Sequence 32, Application US/09548367D  
 Patent No. 6440698  
 GENERAL INFORMATION:  
 APPLICANT: GURNEY ET AL.  
 TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES  
 FILE REFERENCE: 29915/62801  
 CURRENT APPLICATION NUMBER: US/09/548,367D  
 CURRENT FILING DATE: 2000-04-12  
 PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: US 09/404,133  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: PCT/US99/20881  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: US 60/101,594  
; PRIOR FILING DATE: 1998-09-24  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 32  
; LENGTH: 459  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-548-367D-32

Query Match 54.7%; Score 35; DB 4; Length 459;  
Best Local Similarity 44.4%; Pred. No. 4.2e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLM 9  
|||:|  
Db 250 WYPIRREW 258

RESULT 97  
US-09-551-853D-24  
; Sequence 24, Application US/09551853D  
; Patent No. 6500667  
; GENERAL INFORMATION:  
; APPLICANT: GURNEY ET AL.  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES  
; FILE REFERENCE: 29915/6280L  
; CURRENT FILING DATE: 2000-04-18  
; PRIOR APPLICATION NUMBER: US 60/155,493  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: US 09/404,133  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: PCT/US99/20881  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: US 60/101,594  
; PRIOR FILING DATE: 1998-09-24  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 24  
; LENGTH: 459  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-551-853D-24

Query Match 54.7%; Score 35; DB 4; Length 459;  
Best Local Similarity 44.4%; Pred. No. 4.2e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLM 9  
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Db 256 WYPIRREW 264

RESULT 98  
US-09-551-853D-32  
; Sequence 32, Application US/09551853D  
; Patent No. 6500667  
; GENERAL INFORMATION:  
; APPLICANT: GURNEY ET AL.  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES  
; FILE REFERENCE: 29915/6280L  
; CURRENT APPLICATION NUMBER: US/09/551,853D  
; CURRENT FILING DATE: 2000-04-18  
; PRIOR APPLICATION NUMBER: US 60/155,493  
; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: PCT/US99/20881  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: US 60/101,594  
; PRIOR FILING DATE: 1998-09-24  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 32  
; LENGTH: 459  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-551-853D-32

Query Match 54.7%; Score 35; DB 4; Length 459;  
Best Local Similarity 44.4%; Pred. No. 4.2e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLM 9  
|||:|  
Db 250 WYPIRREW 258

RESULT 99  
US-09-548-372D-6  
; Sequence 6, Application US/09548372D  
; Patent No. 6420534  
; GENERAL INFORMATION:  
; APPLICANT: GURNEY ET AL.  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES  
; FILE REFERENCE: 29915/6280I  
; CURRENT APPLICATION NUMBER: US/09/548,372D  
; CURRENT FILING DATE: 2000-04-12  
; PRIOR APPLICATION NUMBER: US 60/155,493  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: US 09/404,133  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: PCT/US99/20881  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: US 60/101,594  
; PRIOR FILING DATE: 1998-09-24  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 476  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-548-372D-6

Query Match 54.7%; Score 35; DB 4; Length 476;  
Best Local Similarity 44.4%; Pred. No. 4.4e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLM 9  
|||:|  
Db 225 WYPIRREW 233

RESULT 100  
US-09-548-372D-73  
; Sequence 73, Application US/09548372D  
; Patent No. 6420534  
; GENERAL INFORMATION:  
; APPLICANT: GURNEY ET AL.  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES  
; FILE REFERENCE: 29915/6280I  
; CURRENT APPLICATION NUMBER: US/09/548,372D  
; CURRENT FILING DATE: 2000-04-12  
; PRIOR APPLICATION NUMBER: US 60/155,493  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23  
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881  
 ; PRIOR FILING DATE: 1999-09-23  
 ; PRIOR APPLICATION NUMBER: US 60/101,594  
 ; PRIOR FILING DATE: 1998-09-24  
 ; NUMBER OF SEQ ID NOS: 73  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO: 73  
 ; LENGTH: 476  
 ; TYPE: prt  
 ; ORGANISM: Mus musculus  
 ; US-09-548-372D-73

Query Match 54.7%; Score 35; DB 4; Length 476;  
 Best Local Similarity 44.4%; Pred. NO. 4.4e+02;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKW 9  
 Db 225 WYTPRRRW 233

Search completed: July 12, 2004, 21:30:18  
 Job time : 26 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 12, 2004, 21:29:57 ; Search time 46 seconds  
(without alignments)  
67,808 Million cell updates/sec

Title: US-09-932-613-457

Perfect score: 64

Sequence: 1 WYDPLTKLWL 10

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1279676 seqs, 311918243 residues

Total number of hits satisfying chosen parameters: 1279676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : Published Applications AA:\*

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3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
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13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
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Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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1	64	100.0	10	10	US-09-932-613-436 Sequence 436, App
2	64	100.0	10	10	US-09-932-613-457 Sequence 457, App
3	64	100.0	10	10	US-09-932-322-436 Sequence 436, App
4	64	100.0	10	10	US-09-932-322-457 Sequence 457, App
5	64	100.0	10	10	US-09-932-613-456 Sequence 456, App
6	64	100.0	12	10	US-09-932-322-456 Sequence 456, App
7	64	100.0	13	10	US-09-932-613-439 Sequence 439, App
8	64	100.0	13	10	US-09-932-322-439 Sequence 439, App
9	64	100.0	14	10	US-09-932-613-186 Sequence 186, App
10	64	100.0	14	10	US-09-932-613-187 Sequence 187, App
11	64	100.0	14	10	US-09-932-613-188 Sequence 188, App
12	64	100.0	14	10	US-09-932-613-189 Sequence 189, App
13	64	100.0	14	10	US-09-932-613-190 Sequence 190, App
14	64	100.0	14	10	US-09-932-613-191 Sequence 191, App
15	64	100.0	14	10	US-09-932-613-192 Sequence 192, App

16	64	100.0	14	10	US-09-932-613-193 Sequence 193, App
17	64	100.0	14	10	US-09-932-613-194 Sequence 194, App
18	64	100.0	14	10	US-09-932-613-195 Sequence 195, App
19	64	100.0	14	10	US-09-932-613-196 Sequence 196, App
20	64	100.0	14	10	US-09-932-613-197 Sequence 197, App
21	64	100.0	14	10	US-09-932-613-198 Sequence 198, App
22	64	100.0	14	10	US-09-932-613-199 Sequence 199, App
23	64	100.0	14	10	US-09-932-613-200 Sequence 200, App
24	64	100.0	14	10	US-09-932-613-201 Sequence 201, App
25	64	100.0	14	10	US-09-932-613-202 Sequence 202, App
26	64	100.0	14	10	US-09-932-613-203 Sequence 203, App
27	64	100.0	14	10	US-09-932-613-204 Sequence 204, App
28	64	100.0	14	10	US-09-932-613-205 Sequence 205, App
29	64	100.0	14	10	US-09-932-613-206 Sequence 206, App
30	64	100.0	14	10	US-09-932-613-207 Sequence 207, App
31	64	100.0	14	10	US-09-932-613-208 Sequence 208, App
32	64	100.0	14	10	US-09-932-613-209 Sequence 209, App
33	64	100.0	14	10	US-09-932-613-210 Sequence 210, App
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35	64	100.0	14	10	US-09-932-613-212 Sequence 212, App
36	64	100.0	14	10	US-09-932-613-213 Sequence 213, App
37	64	100.0	14	10	US-09-932-613-214 Sequence 214, App
38	64	100.0	14	10	US-09-932-613-215 Sequence 215, App
39	64	100.0	14	10	US-09-932-613-216 Sequence 216, App
40	64	100.0	14	10	US-09-932-613-217 Sequence 217, App
41	64	100.0	14	10	US-09-932-613-218 Sequence 218, App
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43	64	100.0	14	10	US-09-932-613-220 Sequence 220, App
44	64	100.0	14	10	US-09-932-613-221 Sequence 221, App
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46	64	100.0	14	10	US-09-932-613-223 Sequence 223, App
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49	64	100.0	14	10	US-09-932-613-226 Sequence 226, App
50	64	100.0	14	10	US-09-932-613-227 Sequence 227, App
51	64	100.0	14	10	US-09-932-613-228 Sequence 228, App
52	64	100.0	14	10	US-09-932-613-229 Sequence 229, App
53	64	100.0	14	10	US-09-932-613-230 Sequence 230, App
54	64	100.0	14	10	US-09-932-613-231 Sequence 231, App
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62	64	100.0	14	10	US-09-932-613-239 Sequence 239, App
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67	64	100.0	14	10	US-09-932-613-244 Sequence 244, App
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84	64	100.0	14	10	US-09-932-613-261 Sequence 261, App
85	64	100.0	14	10	US-09-932-613-262 Sequence 262, App
86	64	100.0	14	10	US-09-932-613-263 Sequence 263, App
87	64	100.0	14	10	US-09-932-613-264 Sequence 264, App
88	64	100.0	14	10	US-09-932-613-265 Sequence 265, App





235	64	100.0	17	10	US-09-932-613-437	Sequence 437, App
236	64	100.0	17	10	US-09-932-613-440	Sequence 440, App
237	64	100.0	17	10	US-09-932-322-437	Sequence 437, App
238	64	100.0	17	10	US-09-932-322-440	Sequence 440, App
239	62	96.9	14	10	US-09-932-613-385	Sequence 385, App
240	62	96.9	14	10	US-09-932-613-386	Sequence 386, App
241	62	96.9	14	10	US-09-932-613-387	Sequence 387, App
242	62	96.9	14	10	US-09-932-613-388	Sequence 388, App
243	62	96.9	14	10	US-09-932-613-389	Sequence 389, App
244	62	96.9	14	10	US-09-932-613-390	Sequence 390, App
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248	62	96.9	14	10	US-09-932-322-388	Sequence 388, App
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256	61	95.3	14	10	US-09-932-613-380	Sequence 380, App
257	61	95.3	14	10	US-09-932-613-381	Sequence 381, App
258	61	95.3	14	10	US-09-932-613-382	Sequence 382, App
259	61	95.3	14	10	US-09-932-613-383	Sequence 383, App
260	61	95.3	14	10	US-09-932-613-384	Sequence 384, App
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269	61	95.3	14	10	US-09-932-322-383	Sequence 383, App
270	61	95.3	14	10	US-09-932-322-384	Sequence 384, App
271	60	93.8	14	10	US-09-932-613-306	Sequence 306, App
272	60	93.8	14	10	US-09-932-613-307	Sequence 307, App
273	60	93.8	14	10	US-09-932-613-308	Sequence 308, App
274	60	93.8	14	10	US-09-932-613-309	Sequence 309, App
275	60	93.8	14	10	US-09-932-613-310	Sequence 310, App
276	60	93.8	14	10	US-09-932-613-311	Sequence 311, App
277	60	93.8	14	10	US-09-932-613-312	Sequence 312, App
278	60	93.8	14	10	US-09-932-613-313	Sequence 313, App
279	60	93.8	14	10	US-09-932-613-314	Sequence 314, App
280	60	93.8	14	10	US-09-932-613-315	Sequence 315, App
281	60	93.8	14	10	US-09-932-613-316	Sequence 316, App
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283	60	93.8	14	10	US-09-932-613-318	Sequence 318, App
284	60	93.8	14	10	US-09-932-613-319	Sequence 319, App
285	60	93.8	14	10	US-09-932-613-320	Sequence 320, App
286	60	93.8	14	10	US-09-932-613-321	Sequence 321, App
287	60	93.8	14	10	US-09-932-613-322	Sequence 322, App
288	60	93.8	14	10	US-09-932-613-323	Sequence 323, App
289	60	93.8	14	10	US-09-932-613-352	Sequence 352, App
290	60	93.8	14	10	US-09-932-613-353	Sequence 353, App
291	60	93.8	14	10	US-09-932-613-354	Sequence 354, App
292	60	93.8	14	10	US-09-932-613-355	Sequence 355, App
293	60	93.8	14	10	US-09-932-613-356	Sequence 356, App
294	60	93.8	14	10	US-09-932-613-357	Sequence 357, App
295	60	93.8	14	10	US-09-932-613-358	Sequence 358, App
296	60	93.8	14	10	US-09-932-613-359	Sequence 359, App
297	60	93.8	14	10	US-09-932-613-360	Sequence 360, App
298	60	93.8	14	10	US-09-932-613-361	Sequence 361, App
299	60	93.8	14	10	US-09-932-613-362	Sequence 362, App
300	60	93.8	14	10	US-09-932-613-363	Sequence 363, App

## ALIGNMENTS

RESULT 1  
US-09-932-613-436

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Sequence 436, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Pottery, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 436
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: core peptide of high affinity Blys binders
US-09-932-613-436

Query Match          100.0%; Score 64; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
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Db 1 WYDPLTKLWL 10

RESULT 2
US-09-932-613-457
; Sequence 457, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Pottery, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 457
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-457

Query Match          100.0%; Score 64; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
   |||||
Db 1 WYDPLTKLWL 10

RESULT 3
US-09-932-322-436
; Sequence 436, Application US/09932322
; Publication No. US20030194743A1
; GENERAL INFORMATION:
; APPLICANT: Dyax Corp.
; APPLICANT: Beltzer, James P.
; APPLICANT: Pottery, M. Daniel
; APPLICANT: Fleming, Tony J.
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; APPLICANT: Ladner, Robert Charles
; TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (Blys)
; FILE REFERENCE: DYX-018.1 PCT; DYX-018.1 US
; CURRENT APPLICATION NUMBER: US/09/932,322
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 436
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: core peptide of high affinity Blys binders
; US-09-932-322-436

Query Match          100.0%; Score 64; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WYDPLTKLWL 10
        |||||
        1 WYDPLTKLWL 10

Db
1 WYDPLTKLWL 10

RESULT 4
US-09-932-322-457
; Sequence 457, Application US/09932322
; Publication No. US20030194743A1
; GENERAL INFORMATION:
; APPLICANT: Dyax Corp.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (Blys)
; FILE REFERENCE: DYX-018.1 PCT; DYX-018.1 US
; CURRENT APPLICATION NUMBER: US/09/932,322
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 457
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
; US-09-932-322-457

Query Match          100.0%; Score 64; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WYDPLTKLWL 10
        |||||
        1 WYDPLTKLWL 10

Db
1 WYDPLTKLWL 10

RESULT 5
US-09-932-613-456
; Sequence 456, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
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; SEQ ID NO 456
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
; US-09-932-613-456

Query Match          100.0%; Score 64; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WYDPLTKLWL 10
        |||||
        1 WYDPLTKLWL 10

Db
1 WYDPLTKLWL 10

RESULT 6
US-09-932-322-456
; Sequence 456, Application US/09932322
; Publication No. US20030194743A1
; GENERAL INFORMATION:
; APPLICANT: Dyax Corp.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Ladner, Robert Charles
; TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (Blys)
; FILE REFERENCE: DYX-018.1 PCT; DYX-018.1 US
; CURRENT APPLICATION NUMBER: US/09/932,322
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 456
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
; US-09-932-322-456

Query Match          100.0%; Score 64; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WYDPLTKLWL 10
        |||||
        1 WYDPLTKLWL 10

Db
1 WYDPLTKLWL 10

RESULT 7
US-09-932-613-439
; Sequence 439, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 439
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
; US-09-932-613-439
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Query Match 100.0%; Score 64; DB 10; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0021;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10  
|||||  
DB 1 WYDPLTKLML 10

RESULT 8  
US-09-932-322-439  
; Sequence 439, Application US/09932322  
; Publication No. US20030194743A1  
; GENERAL INFORMATION:  
; APPLICANT: Dyax Corp.  
; APPLICANT: Beltzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Laderer, Robert Charles  
; TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (Blys)  
; FILE REFERENCE: DYX-018.1 PCT; DYX-018.1 US  
; CURRENT APPLICATION NUMBER: US/09/932.322  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 439  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-322-439

Query Match 100.0%; Score 64; DB 10; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0021;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10  
|||||  
DB 1 WYDPLTKLML 10

RESULT 9  
US-09-932-613-186  
; Sequence 186, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Beltzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932.613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 186  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-186

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10  
|||||

DB 3 WYDPLTKLML 12

RESULT 10  
US-09-932-613-187  
; Sequence 187, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Beltzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932.613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 187  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-187

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10  
|||||  
DB 3 WYDPLTKLML 12

RESULT 11  
US-09-932-613-188  
; Sequence 188, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Beltzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932.613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 188  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-188

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10  
|||||  
DB 3 WYDPLTKLML 12

RESULT 12  
US-09-932-613-189  
; Sequence 189, Application US/09932613  
; Publication No. US20030091565A1

```

; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltez, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: Dyx-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 189
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-189

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
   |||||
   |||||
Db 3 WYDPLTKLWL 12

RESULT 13
US-09-932-613-190
; Sequence 190, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltez, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: Dyx-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 190
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-190

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
   |||||
   |||||
Db 3 WYDPLTKLWL 12

RESULT 14
US-09-932-613-191
; Sequence 191, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltez, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON

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; FILE REFERENCE: Dyx-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 191
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-191

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
   |||||
   |||||
Db 3 WYDPLTKLWL 12

RESULT 15
US-09-932-613-192
; Sequence 192, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltez, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: Dyx-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 192
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-192

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
   |||||
   |||||
Db 3 WYDPLTKLWL 12

RESULT 16
US-09-932-613-193
; Sequence 193, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltez, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: Dyx-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 193
; LENGTH: 14

```

TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-193

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
|||  
Db 3 WYDPLTKLWL 12

RESULT 17  
US-09-932-613-194  
Sequence 194, Application US/09932613  
Publication No. US20030091565A1  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
APPLICANT: Beltzer, James P.  
APPLICANT: Potter, M. Daniel  
APPLICANT: Fleming, Tony J.  
APPLICANT: Rosen, Craig A.  
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
CURRENT APPLICATION NUMBER: US/09/932,613  
CURRENT FILING DATE: 2001-08-17  
NUMBER OF SEQ ID NOS: 458  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 194  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-194

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
|||  
Db 3 WYDPLTKLWL 12

RESULT 18  
US-09-932-613-195  
Sequence 195, Application US/09932613  
Publication No. US20030091565A1  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
APPLICANT: Beltzer, James P.  
APPLICANT: Potter, M. Daniel  
APPLICANT: Fleming, Tony J.  
APPLICANT: Rosen, Craig A.  
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
CURRENT APPLICATION NUMBER: US/09/932,613  
CURRENT FILING DATE: 2001-08-17  
NUMBER OF SEQ ID NOS: 458  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 195  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-195

Query Match 100.0%; Score 64; DB 10; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
|||  
Db 3 WYDPLTKLWL 12

RESULT 19  
US-09-932-613-196  
Sequence 196, Application US/09932613  
Publication No. US20030091565A1  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
APPLICANT: Beltzer, James P.  
APPLICANT: Potter, M. Daniel  
APPLICANT: Fleming, Tony J.  
APPLICANT: Rosen, Craig A.  
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
CURRENT APPLICATION NUMBER: US/09/932,613  
CURRENT FILING DATE: 2001-08-17  
NUMBER OF SEQ ID NOS: 458  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 196  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-196

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
|||  
Db 3 WYDPLTKLWL 12

RESULT 20  
US-09-932-613-197  
Sequence 197, Application US/09932613  
Publication No. US20030091565A1  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
APPLICANT: Beltzer, James P.  
APPLICANT: Potter, M. Daniel  
APPLICANT: Fleming, Tony J.  
APPLICANT: Rosen, Craig A.  
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
CURRENT APPLICATION NUMBER: US/09/932,613  
CURRENT FILING DATE: 2001-08-17  
NUMBER OF SEQ ID NOS: 458  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 197  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-197

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
|||  
Db 3 WYDPLTKLWL 12

RESULT 21  
US-09-932-613-198  
; Sequence 198, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Beltzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 198  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-198

Query Match      100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WYDPLTKLWL 10  
         |||||  
DB      3 WYDPLTKLWL 12

RESULT 22  
US-09-932-613-199  
; Sequence 199, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Beltzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 199  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-199

Query Match      100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WYDPLTKLWL 10  
         |||||  
DB      3 WYDPLTKLWL 12

RESULT 23  
US-09-932-613-200  
; Sequence 200, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.

; APPLICANT: Beltzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 200  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-200

Query Match      100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WYDPLTKLWL 10  
         |||||  
DB      3 WYDPLTKLWL 12

RESULT 24  
US-09-932-613-201  
; Sequence 201, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Beltzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 201  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-201

Query Match      100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WYDPLTKLWL 10  
         |||||  
DB      3 WYDPLTKLWL 12

RESULT 25  
US-09-932-613-202  
; Sequence 202, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Beltzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,613

```

; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 202
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-202

Query Match
Best Local Similarity 100.0%; Score 64; DB 10; Length 14;
Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
   |||||
Db 3 WYDPLTKLML 12

RESULT 26
US-09-932-613-203
; Sequence 203, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 203
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-203

Query Match
Best Local Similarity 100.0%; Score 64; DB 10; Length 14;
Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
   |||||
Db 3 WYDPLTKLML 12

RESULT 27
US-09-932-613-204
; Sequence 204, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 204
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
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```

; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-204

Query Match
Best Local Similarity 100.0%; Score 64; DB 10; Length 14;
Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
   |||||
Db 3 WYDPLTKLML 12

RESULT 28
US-09-932-613-205
; Sequence 205, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 205
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-205

Query Match
Best Local Similarity 100.0%; Score 64; DB 10; Length 14;
Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10
   |||||
Db 3 WYDPLTKLML 12

RESULT 29
US-09-932-613-206
; Sequence 206, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 206
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-206

Query Match
Best Local Similarity 100.0%; Score 64; DB 10; Length 14;
Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 WYDPLTKLML 10  
| | | | |  
Db 3 WYDPLTKLML 12

## RESULT 30

US-09-932-613-207  
; Sequence 207, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Beltzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 207  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-207

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10  
| | | | |  
Db 3 WYDPLTKLML 12

## RESULT 31

US-09-932-613-208  
; Sequence 208, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Beltzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 208  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-208

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10  
| | | | |  
Db 3 WYDPLTKLML 12

## RESULT 32

US-09-932-613-209  
; Sequence 209, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Beltzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 209  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-209

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10  
| | | | |  
Db 3 WYDPLTKLML 12

## RESULT 33

US-09-932-613-210  
; Sequence 210, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Beltzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 210  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-210

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10  
| | | | |  
Db 3 WYDPLTKLML 12

## RESULT 34

US-09-932-613-211  
; Sequence 211, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Beltzer, James P.  
; APPLICANT: Potter, M. Daniel



```

; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 211
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-211

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WYDPLTKLML 10
        |||||
Db      3 WYDPLTKLML 12

RESULT 35
US-09-932-613-212
; Sequence 212, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 212
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-212

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WYDPLTKLML 10
        |||||
Db      3 WYDPLTKLML 12

RESULT 36
US-09-932-613-213
; Sequence 213, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 213
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-213
```

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 213
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-213

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WYDPLTKLML 10
        |||||
Db      3 WYDPLTKLML 12

RESULT 37
US-09-932-613-214
; Sequence 214, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 214
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-214

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WYDPLTKLML 10
        |||||
Db      3 WYDPLTKLML 12

RESULT 38
US-09-932-613-215
; Sequence 215, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 215
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-215
```

US-09-932-613-215

Query Match  
Best Local Similarity 100.0%; Score 64; DB 10; Length 14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
|||||  
3 WYDPLTKLWL 12

RESULT 39

US-09-932-613-216  
; Sequence 216, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Belzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 216  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-216

Query Match  
Best Local Similarity 100.0%; Score 64; DB 10; Length 14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
|||||  
3 WYDPLTKLWL 12

RESULT 40

US-09-932-613-217  
; Sequence 217, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Belzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 217  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-217

Query Match  
Best Local Similarity 100.0%; Score 64; DB 10; Length 14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10

Db 3 WYDPLTKLWL 12  
|||||

RESULT 41  
US-09-932-613-218  
; Sequence 218, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Belzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 218  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-218

Query Match  
Best Local Similarity 100.0%; Score 64; DB 10; Length 14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
|||||  
3 WYDPLTKLWL 12

RESULT 42  
US-09-932-613-219  
; Sequence 219, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Belzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 219  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-219

Query Match  
Best Local Similarity 100.0%; Score 64; DB 10; Length 14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
|||||  
3 WYDPLTKLWL 12

RESULT 43  
US-09-932-613-220  
; Sequence 220, Application US/09932613

```

; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 220
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-220

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLML 10
Db 3 WYDPLTKLML 12

RESULT 44
US-09-932-613-221
; Sequence 221, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 221
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-221

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLML 10
Db 3 WYDPLTKLML 12

RESULT 45
US-09-932-613-222
; Sequence 222, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
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; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 222
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-222

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLML 10
Db 3 WYDPLTKLML 12

RESULT 46
US-09-932-613-223
; Sequence 223, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 223
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-223

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLML 10
Db 3 WYDPLTKLML 12

RESULT 47
US-09-932-613-224
; Sequence 224, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 224
```

LENGTH: 14  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Blys binding polypeptide  
 US-09-932-613-224

Query Match 100.0%; Score 64; DB 10; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.0022;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
 |||||  
 DB 3 WYDPLTKLWL 12

RESULT 48  
 US-09-932-613-225  
 Sequence 225, Application US/09932613  
 Publication No. US20030091565A1  
 GENERAL INFORMATION:  
 APPLICANT: Human Genome Sciences, Inc.  
 APPLICANT: Beltzer, James P.  
 APPLICANT: Potter, M. Daniel  
 APPLICANT: Fleming, Tony J.  
 APPLICANT: Rosen, Craig A.  
 TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
 FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
 CURRENT FILING DATE: 2001-08-17  
 NUMBER OF SEQ ID NOS: 458  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 225  
 LENGTH: 14  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Blys binding polypeptide  
 US-09-932-613-225

Query Match 100.0%; Score 64; DB 10; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.0022;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
 |||||  
 DB 3 WYDPLTKLWL 12

RESULT 49  
 US-09-932-613-226  
 Sequence 226, Application US/09932613  
 Publication No. US20030091565A1  
 GENERAL INFORMATION:  
 APPLICANT: Human Genome Sciences, Inc.  
 APPLICANT: Beltzer, James P.  
 APPLICANT: Potter, M. Daniel  
 APPLICANT: Fleming, Tony J.  
 APPLICANT: Rosen, Craig A.  
 TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
 FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
 CURRENT FILING DATE: 2001-08-17  
 NUMBER OF SEQ ID NOS: 458  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 226  
 LENGTH: 14  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Blys binding polypeptide  
 US-09-932-613-226

Query Match 100.0%; Score 64; DB 10; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.0022;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
 |||||  
 DB 3 WYDPLTKLWL 12

RESULT 50  
 US-09-932-613-227  
 Sequence 227, Application US/09932613  
 Publication No. US20030091565A1  
 GENERAL INFORMATION:  
 APPLICANT: Human Genome Sciences, Inc.  
 APPLICANT: Beltzer, James P.  
 APPLICANT: Potter, M. Daniel  
 APPLICANT: Fleming, Tony J.  
 APPLICANT: Rosen, Craig A.  
 TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
 FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
 CURRENT FILING DATE: 2001-08-17  
 NUMBER OF SEQ ID NOS: 458  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 227  
 LENGTH: 14  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Blys binding polypeptide  
 US-09-932-613-227

Query Match 100.0%; Score 64; DB 10; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.0022;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
 |||||  
 DB 3 WYDPLTKLWL 12

RESULT 51  
 US-09-932-613-228  
 Sequence 228, Application US/09932613  
 Publication No. US20030091565A1  
 GENERAL INFORMATION:  
 APPLICANT: Human Genome Sciences, Inc.  
 APPLICANT: Beltzer, James P.  
 APPLICANT: Potter, M. Daniel  
 APPLICANT: Fleming, Tony J.  
 APPLICANT: Rosen, Craig A.  
 TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
 FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
 CURRENT FILING DATE: 2001-08-17  
 NUMBER OF SEQ ID NOS: 458  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 228  
 LENGTH: 14  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Blys binding polypeptide  
 US-09-932-613-228

Query Match 100.0%; Score 64; DB 10; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.0022;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
 |||||  
 DB 3 WYDPLTKLWL 12

```
RESULT 52
US-09-932-613-229
; Sequence 229, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 229
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-229

Query Match      100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLWL 10
        |||||
Db      3 WYDPLTKLWL 12

RESULT 53
US-09-932-613-230
; Sequence 230, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 230
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-230

Query Match      100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLWL 10
        |||||
Db      3 WYDPLTKLWL 12

RESULT 54
US-09-932-613-231
; Sequence 231, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 231
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-231

Query Match      100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLWL 10
        |||||
Db      3 WYDPLTKLWL 12

RESULT 55
US-09-932-613-232
; Sequence 232, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 232
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-232

Query Match      100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLWL 10
        |||||
Db      3 WYDPLTKLWL 12

RESULT 56
US-09-932-613-233
; Sequence 233, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
```

;;  
;; CURRENT APPLICATION NUMBER: US/09/932,613  
;; CURRENT FILING DATE: 2001-08-17  
;; NUMBER OF SEQ ID NOS: 458  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 233  
;; LENGTH: 14  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-233

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
Db 3 WYDPLTKLWL 12

RESULT 57  
US-09-932-613-234  
; Sequence 234, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Beltzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 234  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-234

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
Db 3 WYDPLTKLWL 12

RESULT 58  
US-09-932-613-235  
; Sequence 235, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Beltzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 235  
; LENGTH: 14  
; TYPE: PRT

;;  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-235

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
Db 3 WYDPLTKLWL 12

RESULT 59  
US-09-932-613-236  
; Sequence 236, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Beltzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 236  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-236

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
Db 3 WYDPLTKLWL 12

RESULT 60  
US-09-932-613-237  
; Sequence 237, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Beltzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 237  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-237

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10  
| | | | |  
Db 3 WYDPLTKLWL 12

## RESULT 61

US-09-932-613-238  
; Sequence 238, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Beltzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT FILING DATE: 2001-08-17  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 238  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-238

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10  
| | | | |  
Db 3 WYDPLTKLWL 12

## RESULT 62

US-09-932-613-239  
; Sequence 239, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Beltzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT FILING DATE: 2001-08-17  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 239  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-239

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10  
| | | | |  
Db 3 WYDPLTKLWL 12

## RESULT 63

US-09-932-613-240  
; Sequence 240, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Beltzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT FILING DATE: 2001-08-17  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 240  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-240

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10  
| | | | |  
Db 3 WYDPLTKLWL 12

## RESULT 64

US-09-932-613-241  
; Sequence 241, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Beltzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT FILING DATE: 2001-08-17  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 241  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-241

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10  
| | | | |  
Db 3 WYDPLTKLWL 12

## RESULT 65

US-09-932-613-242  
; Sequence 242, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Beltzer, James P.

```

; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 242
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-242

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLWL 10
        |||||
Db      3 WYDPLTKLWL 12

RESULT 66
US-09-932-613-243
; Sequence 243, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 243
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-243

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLWL 10
        |||||
Db      3 WYDPLTKLWL 12

RESULT 67
US-09-932-613-244
; Sequence 244, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
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; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 244
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-244

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLWL 10
        |||||
Db      3 WYDPLTKLWL 12

RESULT 68
US-09-932-613-245
; Sequence 245, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 245
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-245

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLWL 10
        |||||
Db      3 WYDPLTKLWL 12

RESULT 69
US-09-932-613-246
; Sequence 246, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 246
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-246

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLWL 10  
|||  
DB 3 WYDPLTKLWL 12

RESULT 70  
US-09-932-613-247

Sequence 247, Application US/09932613  
Publication No. US20030091565A1  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.

APPLICANT: Beltzer, James P.  
APPLICANT: Potter, M. Daniel  
APPLICANT: Fleming, Tony J.

APPLICANT: Rosen, Craig A.

TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US

CURRENT APPLICATION NUMBER: US/09/932,613  
CURRENT FILING DATE: 2001-08-17

NUMBER OF SEQ ID NOS: 458  
SOFTWARE: PatentIn version 3.1

SEQ ID NO 247

LENGTH: 14

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Blys binding polypeptide

US-09-932-613-247

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLWL 10  
|||  
DB 3 WYDPLTKLWL 12

RESULT 71  
US-09-932-613-248

Sequence 248, Application US/09932613  
Publication No. US20030091565A1  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.

APPLICANT: Beltzer, James P.  
APPLICANT: Potter, M. Daniel  
APPLICANT: Fleming, Tony J.

APPLICANT: Rosen, Craig A.

TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US

CURRENT APPLICATION NUMBER: US/09/932,613  
CURRENT FILING DATE: 2001-08-17

NUMBER OF SEQ ID NOS: 458  
SOFTWARE: PatentIn version 3.1

SEQ ID NO 248

LENGTH: 14

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Blys binding polypeptide

US-09-932-613-248

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLWL 10  
|||  
DB 3 WYDPLTKLWL 12

RESULT 72  
US-09-932-613-249

Sequence 249, Application US/09932613  
Publication No. US20030091565A1  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.

APPLICANT: Beltzer, James P.  
APPLICANT: Potter, M. Daniel  
APPLICANT: Fleming, Tony J.

APPLICANT: Rosen, Craig A.

TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US

CURRENT APPLICATION NUMBER: US/09/932,613  
CURRENT FILING DATE: 2001-08-17

NUMBER OF SEQ ID NOS: 458  
SOFTWARE: PatentIn version 3.1

SEQ ID NO 249

LENGTH: 14

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Blys binding polypeptide

US-09-932-613-249

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLWL 10  
|||  
DB 3 WYDPLTKLWL 12

RESULT 73  
US-09-932-613-250

Sequence 250, Application US/09932613  
Publication No. US20030091565A1  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.

APPLICANT: Beltzer, James P.  
APPLICANT: Potter, M. Daniel  
APPLICANT: Fleming, Tony J.

APPLICANT: Rosen, Craig A.

TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US

CURRENT APPLICATION NUMBER: US/09/932,613  
CURRENT FILING DATE: 2001-08-17

NUMBER OF SEQ ID NOS: 458  
SOFTWARE: PatentIn version 3.1

SEQ ID NO 250

LENGTH: 14

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Blys binding polypeptide

US-09-932-613-250

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPLTKLWL 10  
|||  
DB 3 WYDPLTKLWL 12

RESULT 74  
US-09-932-613-251

```
; Sequence 251, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: Dyx-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 251
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-251

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
   |||||
Db 3 WYDPLTKLWL 12

RESULT 75
US-09-932-613-252
; Sequence 252, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: Dyx-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 252
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-252

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
   |||||
Db 3 WYDPLTKLWL 12

RESULT 76
US-09-932-613-253
; Sequence 253, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
```

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; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: Dyx-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 253
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-253

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
   |||||
Db 3 WYDPLTKLWL 12

RESULT 77
US-09-932-613-254
; Sequence 254, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: Dyx-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 254
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-254

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
   |||||
Db 3 WYDPLTKLWL 12

RESULT 78
US-09-932-613-255
; Sequence 255, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: Dyx-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
```

SEQ ID NO 255  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-255

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10  
|||  
Db 3 WYDPLTKLML 12

RESULT 79  
US-09-932-613-256  
Sequence 256, Application US/09932613  
Publication No. US20030091565A1  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
APPLICANT: Beltzer, James P.  
APPLICANT: Potter, M. Daniel  
APPLICANT: Fleming, Tony J.  
APPLICANT: Rosen, Craig A.  
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
CURRENT APPLICATION NUMBER: US/09/932,613  
CURRENT FILING DATE: 2001-08-17  
NUMBER OF SEQ ID NOS: 458  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 256  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-256

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10  
|||  
Db 3 WYDPLTKLML 12

RESULT 80  
US-09-932-613-257  
Sequence 257, Application US/09932613  
Publication No. US20030091565A1  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
APPLICANT: Beltzer, James P.  
APPLICANT: Potter, M. Daniel  
APPLICANT: Fleming, Tony J.  
APPLICANT: Rosen, Craig A.  
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
CURRENT APPLICATION NUMBER: US/09/932,613  
CURRENT FILING DATE: 2001-08-17  
NUMBER OF SEQ ID NOS: 458  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 257  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-257

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10  
|||  
Db 3 WYDPLTKLML 12

RESULT 81  
US-09-932-613-258  
Sequence 258, Application US/09932613  
Publication No. US20030091565A1  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
APPLICANT: Beltzer, James P.  
APPLICANT: Potter, M. Daniel  
APPLICANT: Fleming, Tony J.  
APPLICANT: Rosen, Craig A.  
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
CURRENT APPLICATION NUMBER: US/09/932,613  
CURRENT FILING DATE: 2001-08-17  
NUMBER OF SEQ ID NOS: 458  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 258  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-258

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10  
|||  
Db 3 WYDPLTKLML 12

RESULT 82  
US-09-932-613-259  
Sequence 259, Application US/09932613  
Publication No. US20030091565A1  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
APPLICANT: Beltzer, James P.  
APPLICANT: Potter, M. Daniel  
APPLICANT: Fleming, Tony J.  
APPLICANT: Rosen, Craig A.  
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
CURRENT APPLICATION NUMBER: US/09/932,613  
CURRENT FILING DATE: 2001-08-17  
NUMBER OF SEQ ID NOS: 458  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 259  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-259

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLML 10  
|||

Db 3 WYDPLTKLWL 12

RESULT 83  
US-09-932-613-260  
; Sequence 260, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Belzter, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 260  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-260

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
| | | | | | | | | |  
Db 3 WYDPLTKLWL 12

RESULT 84  
US-09-932-613-261  
; Sequence 261, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Belzter, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 261  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-261

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
| | | | | | | | | |  
Db 3 WYDPLTKLWL 12

RESULT 85  
US-09-932-613-262  
; Sequence 262, Application US/09932613  
; Publication No. US20030091565A1

; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Belzter, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 262  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-262

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
| | | | | | | | | |  
Db 3 WYDPLTKLWL 12

RESULT 86  
US-09-932-613-263  
; Sequence 263, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Belzter, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 263  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-263

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
| | | | | | | | | |  
Db 3 WYDPLTKLWL 12

RESULT 87  
US-09-932-613-264  
; Sequence 264, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Belzter, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON

```
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 264
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
US-09-932-613-264

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
   |||||
   |||||
Db 3 WYDPLTKLWL 12

RESULT 88
US-09-932-613-265
Sequence 265, Application US/09932613
Publication No. US20030091565A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Beltzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 265
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-265

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
   |||||
   |||||
Db 3 WYDPLTKLWL 12

RESULT 89
US-09-932-613-266
Sequence 266, Application US/09932613
Publication No. US20030091565A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Beltzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 266
LENGTH: 14
```

```
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-266

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
   |||||
   |||||
Db 3 WYDPLTKLWL 12

RESULT 90
US-09-932-613-267
Sequence 267, Application US/09932613
Publication No. US20030091565A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Beltzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 267
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-267

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
   |||||
   |||||
Db 3 WYDPLTKLWL 12

RESULT 91
US-09-932-613-268
Sequence 268, Application US/09932613
Publication No. US20030091565A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Beltzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 268
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-268

Query Match          100.0%; Score 64; DB 10; Length 14;
```

Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10  
| | | | | | | |  
Db 3 WYDPLTKLWL 12

## RESULT 92

US-09-932-613-269  
; Sequence 269, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Belzter, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 269  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-269

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10  
| | | | | | | |  
Db 3 WYDPLTKLWL 12

## RESULT 93

US-09-932-613-270  
; Sequence 270, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Belzter, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 270  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-270

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10  
| | | | | | | |  
Db 3 WYDPLTKLWL 12

RESULT 94  
US-09-932-613-271

; Sequence 271, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Belzter, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 271  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-271

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10  
| | | | | | | |  
Db 3 WYDPLTKLWL 12

## RESULT 95

US-09-932-613-272  
; Sequence 272, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Belzter, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 272  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-272

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10  
| | | | | | | |  
Db 3 WYDPLTKLWL 12

## RESULT 96

US-09-932-613-273  
; Sequence 273, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.

```

; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 273
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-273

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLML 10
        |||||
        3 WYDPLTKLML 12

RESULT 97
US-09-932-613-274
; Sequence 274, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 274
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-274

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLML 10
        |||||
        3 WYDPLTKLML 12

RESULT 98
US-09-932-613-275
; Sequence 275, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 275
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-275

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLML 10
        |||||
        3 WYDPLTKLML 12
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; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 275
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-275

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLML 10
        |||||
        3 WYDPLTKLML 12

RESULT 99
US-09-932-613-276
; Sequence 276, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 276
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-276

Query Match          100.0%; Score 64; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WYDPLTKLML 10
        |||||
        3 WYDPLTKLML 12

RESULT 100
US-09-932-613-277
; Sequence 277, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 277
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-932-613-277
```

FEATURE:  
; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-277

Query Match 100.0%; Score 64; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. NO. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
|||  
Db 3 WYDPLTKLWL 12

Search completed: July 12, 2004, 21:35:38  
Job time : 47 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 12, 2004, 21:27:27 ; Search time 20 Seconds

(without alignments)  
48.096 Million cell updates/sec

Title: US-09-932-613-457

Perfect score: 64

Sequence: 1 WYDPLTKML 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	71.9	870	1 GNMVUA	pol polypeptide -
2	45	70.3	383	2 B84608	hypothetical prote
3	45	70.3	482	2 G83928	hypothetical prote
4	43	67.2	567	2 AC0754	probable membrane
5	43	67.2	570	2 T20166	hypothetical prote
6	43	67.2	888	1 GNLJHD	pol polypeptide -
7	42	65.6	293	2 T05419	hypothetical prote
8	42	65.6	374	2 B85421	probable polypepti
9	42	65.6	374	2 T04672	polypeptide
10	42	65.6	392	2 T09371	hypothetical prote
11	41	64.1	655	2 F82138	GGBP family prote
12	41	64.1	672	2 H83315	hypothetical prote
13	40	62.5	202	2 S16442	MTP protein - mou
14	40	62.5	345	2 A43586	hypothetical prote
15	40	62.5	378	2 T47407	hypothetical prote
16	40	62.5	519	2 B87353	hypothetical prote
17	39	60.9	157	2 S49622	circ protein - Rho
18	39	60.9	158	2 A57438	tryptophan-rich se
19	39	60.9	176	1 F64725	probable NAD(P)H2
20	39	60.9	176	2 A85486	probable NAD(P)H o
21	39	60.9	176	2 A90635	probable NAD(P)H o
22	39	60.9	176	2 A10512	probable NAD(P)H o
23	39	60.9	308	1 MMLJ51	bel-1 protein - si
24	39	60.9	311	2 S18740	bell protein - sim
25	39	60.9	333	2 S42424	hypothetical prote
26	39	60.9	335	2 T46319	hypothetical prote
27	39	60.9	365	2 T08577	hypothetical prote
28	39	60.9	430	2 T20170	hypothetical prote
29	39	60.9	480	2 T20168	hypothetical prote

30	39	60.9	551	2 D71969	1-lactate permease
31	39	60.9	551	2 E64537	probable integral
32	39	60.9	983	2 E86989	hypothetical prote
33	39	60.9	2183	2 T37218	hypothetical prote
34	38	59.4	190	2 B83990	hypothetical prote
35	38	59.4	206	2 G69057	hypothetical prote
36	38	59.4	295	2 T32202	hypothetical prote
37	38	59.4	321	2 T50966	hypothetical prote
38	38	59.4	341	2 B83298	conserved hypothet
39	38	59.4	361	2 A13513	ATPase virB11 homo
40	38	59.4	380	2 T00683	glucose-6-phosphat
41	38	59.4	491	2 AC2650	glucose-6-phosphat
42	38	59.4	503	2 B97432	1-lactate permease
43	38	59.4	549	2 D14537	L-lactate permease
44	38	59.4	560	2 F81423	L-lactate permease
45	38	59.4	803	2 F90485	hypothetical prote
46	38	59.4	849	2 T46253	hypothetical prote
47	38	59.4	888	2 T51593	GTP-binding regula
48	38	59.4	901	2 T01135	probable GTP-bind
49	38	59.4	1195	2 S76592	5-methyltetrahydro
50	38	59.4	1895	2 T15881	hypothetical prote
51	38	59.4	2825	2 T14271	Doc4 protein, stre
52	38	59.4	2825	2 A70865	hypothetical prote
53	37.5	58.6	227	2 B87102	conserved hypothet
54	37.5	58.6	227	2 C40626	dihydrodipicolinat
55	37.5	58.6	301	1 C40626	hypothetical prote
56	37	57.8	151	2 H87263	partial probable s
57	37	57.8	177	2 B85833	partial probable s
58	37	57.8	166	2 B90988	conserved hypothet
59	37	57.8	266	2 AB0665	conserved hypothet
60	37	57.8	315	2 B69751	hypothetical prote
61	37	57.8	316	2 T15395	hypothetical prote
62	37	57.8	349	2 S67858	gun1 protein - Xan
63	37	57.8	356	2 B82902	citrate-dependent
64	37	57.8	357	2 A95326	probable AtcC [imp
65	37	57.8	363	1 BVBK2	MAK32 protein - Ye
66	37	57.8	383	1 S42003	sterol 24-C-methyl
67	37	57.8	384	2 T19377	conserved hypothet
68	37	57.8	388	2 AHI950	cardamoyl phosphat
69	37	57.8	401	2 B87503	acyl-CoA dehydroge
70	37	57.8	436	2 H87793	protein C27A12.8 [
71	37	57.8	606	2 A72429	oligopeptide ABC t
72	37	57.8	608	2 D72306	hypothetical prote
73	37	57.8	660	2 H71376	probable tpr prote
74	37	57.8	681	2 UX0338	rabphilin-3A - mou
75	37	57.8	784	2 I58166	rabphilin-3A - rat
76	37	57.8	804	2 A48097	rabphilin-3A - bov
77	37	57.8	819	2 A53714	protein kinase (EC
78	37	57.8	872	2 T37789	Scd1 protein - fis
79	37	57.8	965	2 T12545	hypothetical prote
80	37	57.8	985	1 DUBB11	DNA-directed DNA p
81	37	57.8	1105	2 B64973	yeag protein - Bac
82	37	57.8	1337	2 T30291	dextranase - Strept
83	36.5	57.0	222	2 C75250	hypothetical prote
84	36.5	57.0	723	2 B87706	prolyl oligopeptid
85	36.5	57.0	867	2 S72842	methionine synthas
86	36.5	57.0	1206	2 B87072	hypothetical prote
87	36	56.2	205	2 AG1129	hypothetical prote
88	36	56.2	209	2 T16669	pregnancy-specific
89	36	56.2	312	2 T50960	related to nodulat
90	36	56.2	317	2 D64233	hypothetical prote
91	36	56.2	321	2 S59388	probable membrane
92	36	56.2	405	2 H82632	ATPase Xr1828 [imp
93	36	56.2	418	2 T47818	hypothetical prote
94	36	56.2	419	2 S51715	hypothetical prote
95	36	56.2	424	2 F71488	hypothetical prote
96	36	56.2	427	2 A64945	probable membrane
97	36	56.2	427	2 C85795	hypothetical prote
98	36	56.2	427	2 G80946	probable membrane
99	36	56.2	428	2 JQ1864	hypothetical 47.0K
100	36	56.2	460	2 G82847	hypothetical prote
101	36	56.2	531	2 T33099	hypothetical prote
102	36	56.2	540	2 T20352	hypothetical prote



249 34 53.1 547 2 AG1813  
250 34 53.1 551 2 D69282  
251 34 53.1 551 2 A49904  
252 34 53.1 551 2 A98189  
253 34 53.1 551 2 B86036  
254 34 53.1 551 2 AB0976  
255 34 53.1 570 2 T24152  
256 34 53.1 579 2 H88478  
257 34 53.1 613 2 T36922  
258 34 53.1 621 2 AH2257  
259 34 53.1 625 2 T25373  
260 34 53.1 645 2 S49570  
261 34 53.1 668 2 P81101  
262 34 53.1 668 2 G81839  
263 34 53.1 680 2 AB1875  
264 34 53.1 736 2 AB6171  
265 34 53.1 753 2 B96772  
266 34 53.1 800 1 J50029  
267 34 53.1 800 2 B59106  
268 34 53.1 803 2 T10060  
269 34 53.1 809 2 E71660  
270 34 53.1 820 2 G82168  
271 34 53.1 848 2 B86443  
272 34 53.1 868 2 D69297  
273 34 53.1 885 2 G91080  
274 34 53.1 899 2 H85925  
275 34 53.1 1044 2 H97186  
276 34 53.1 1051 2 T43253  
277 34 53.1 1097 2 G85092  
278 34 53.1 1154 2 A39577  
279 34 53.1 1178 2 AD1845  
280 34 53.1 1271 2 TYH08R  
281 34 53.1 1578 2 S76238  
282 34 53.1 1877 2 T40550  
283 34 53.1 2731 1 VFHJH  
284 34 53.1 2733 2 S15760  
285 34 53.1 5005 2 P82884  
286 33.5 52.3 403 2 P83092  
287 33.5 52.3 532 2 S27372  
288 33.5 52.3 556 2 S39297  
289 33.5 52.3 587 2 S33951  
290 33.5 52.3 1529 2 A59189  
291 33 51.6 98 2 T12887  
292 33 51.6 99 2 S72162  
293 33 51.6 103 2 A72134  
294 33 51.6 141 2 T49659  
295 33 51.6 158 2 B87271  
296 33 51.6 182 2 S03445  
297 33 51.6 183 2 A56579  
298 33 51.6 201 2 A82235  
299 33 51.6 202 2 S53980  
300 33 51.6 203 2 S19714

## ALIGNMENTS

RESULT 1  
GNMVVA  
pol polyprotein - sheep pulmonary adenomatosis virus  
N:Contains: endonuclease (EC 3.1.-.-): RNA-directed DNA polymerase (EC 2.7.7.49)  
C:Species: sheep pulmonary adenomatosis virus  
C>Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 08-Apr-1994  
C/Accession: C42740  
R:York, D.F.; Vigne, R.; Verwoerd, D.W.; Querat, G.  
J. Virol. 66, 4930-4939, 1992  
A:Title: Nucleotide sequence of the jaagsiekte retrovirus, an exogenous and endogenous  
A:Reference number: A42740; MUID:9233675; PMID:162959  
A:Accession: C42740  
A:Molecule type: genomic RNA  
A:Residues: 1-870 <YOR>  
A:Cross-references: GB:M60216  
C:Comment: This protein is likely to be expressed as a gag-pol polyprotein.

C:Comment: The precise boundary between RNA-directed DNA polymerase and endonuclease has  
C:Genetics:  
A:Gene: pol  
A:Start codon: UCA  
C:Superfamily: pol polyprotein  
C:KeyWords: endonuclease; hydrolase; nucleotidyltransferase; polypotein; reverse transcri

Query Match 71.9%; Score 46; DB 1; Length 870;  
Best Local Similarity 77.8%; Pred. No. 6.5;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 WYDPLTKLM 9  
Db 813 WKDPLTNLM 821

## RESULT 2

B84608  
hypothetical protein At2g22030 (imported) - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 14-Jul-2003  
C/Accession: B84608  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanhaken, S.E.; Umayam, L.; Tallon, L.  
euss, D.; Nieman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: B84608  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-383 <STO>  
A:Cross-references: GB:AE02093; NID:94587593; PIDN:ADD2621.1; GSPDB:GN00139  
A:Genetics:  
A:Gene: At2g22030  
A:Map position: 2  
C:Superfamily: conserved hypothetical protein containing F-box and Kelch domains

Query Match 70.3%; Score 45; DB 2; Length 383;  
Best Local Similarity 66.7%; Pred. No. 4.1;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 WYDPLTKLM 9  
Db 288 WYDPKDQVM 296

## RESULT 3

G83928  
hypothetical protein BH2231 (imported) - Bacillus halodurans (strain C-125)  
C:Species: Bacillus halodurans  
C>Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
C/Accession: G83928  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A:Reference number: A83650; MUID:20512582; PMID:11058132  
A:Accession: G83928  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-482 <STO>  
A:Cross-references: GB:AP001514; GB:BA000004; NID:910174613; PIDN:BA05950.1; GSPDB:GN001  
A:Experimental source: strain C-125  
A:Genetics:  
A:Gene: BH2231

Query Match 70.3%; Score 45; DB 2; Length 482;  
Best Local Similarity 77.8%; Pred. No. 5.2;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 WYDPLTKLM 9  
Db 443 WYRPLTVLM 451

```

RESULT 4
AC0754
probable membrane protein SRY2194 [imported] - Salmonella enterica subsp. enterica serov.
C/Species: Salmonella enterica subsp. enterica serovar Typhimurium
A/Note: This species has also been called Salmonella typhi
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C/Accession: AC0754
R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,
Th., T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Mole, S.; O'Garra, P.
Nucleotide 433, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov.
A/Reference number: AB0502; PMID:21534947; PMID:11677608
A/Accession: AC0754
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-567 <PAR>
A/Cross-references: GB:AL513382; PIDN:CAD05734.1; PID:g16503227; GSPDB:GN00176
C/genetics:
A/Gene: SRY2194

QY      1 WYDPLTKLW 9
        |||||:|:
DB       396 WHDPILRLV 404

Query Match          67.2%; Score 43; DB 2; Length 567;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
T20166
hypothetical protein CS3A5_6 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T20166
R/Mortimore, B.
submitted to the EMBL Data Library, November 1996
A/Reference number: Z19232
A/Accession: T20166
A>Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-570 <WTL>
A/Cross-references: EMBL:Z81486; PIDN:CAE03987.1; GSPDB:GN00023; CESP:CS3A5_6
A/Experimental source: clone CS3A5
C/Genetics:
A/Gene: CESP:CS3A5_6
A/Map position: 5
A/Introns: 17/1; 86/3; 290/1; 360/3; 428/1

Query March          67.2%; Score 43; DB 2; Length 570;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 YDPLTKLW 9
        |||||
DB       492 YDPLTKSW 499

RESULT 6
GMLJHD
pol polyprotein - squirrel monkey retrovirus SMRV-H (SMRV-HLB)
N/Contains: endonuclease (EC 3.1.-.-); RNA-directed DNA polymerase (EC 2.7.7.49)
C/Species: squirrel monkey retrovirus SMRV-H
C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 01-May-1998
C/Accession: CJ31827
R/Oda, T.; Ikeda, S.; Watanabe, S.; Hatsushika, M.; Akiyama, K.; Mitsunobu, F.
Virology 167, 468-476, 1998
A>Title: Molecular cloning, complete nucleotide sequence, and gene structure of the pr
A/Reference number: AJ31827; PMID:89073750; PMID:3201749

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```

A:Accession: C31827
A:Molecule type: DNA
A:Residues: 1-888 <ODA>
C:Comment: The pol polypeptide contains reverse transcriptase and endonuclease; however,
C:Genetics:
A:Gene: pol
C:Superfamily: pol polypeptide
C:Keywords: endonuclease; hydrolase; nucleotidyltransferase; polypeptide; reverse transcriptase
Query Match      67.2%; Score 43; DB 1; Length 888;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 WYDPLTKLM 9
| | | | | : |
| | | | | : |
Db 821 WRDPLTSVW 829

RESULT 7
T05419
Hypothetical protein F28A23.70 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #ext_change 21-Jul-2003
C:Accession: T05419
R:Bevan, M.; Weichselgartner, M.; Partmann, B.; Granderath, K.; Dauner, D.; Herzl, A.; Ne
submitted to the Protein Sequence Database, October 1998
A:Reference number: Z15415
A:Accession: T05419
A:Molecule type: DNA
A:Residues: 1-293 <BEV>
A:Cross-references: EMBL:AL021961
A:Experimental source: cultivar Columbia; BAC clone F28A23
C:Genetics:
A:Map position: 4
A:Introns: 66/3
A:Notes: F28A23.70
C:Superfamily: conserved hypothetical protein containing F-box and Kelch domains

Query Match      65.6%; Score 42; DB 2; Length 293;
Best Local Similarity 55.6%; Pred. No. 10;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 WYDPLTKLM 9
| | | | | : |
| | | | | : |
Db 244 WYDPKERW 252

RESULT 8
B85421
Probable polygalacturonase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #ext_change 02-Mar-2001
C:Accession: B85421
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Native 402, 765-777, 1999
A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: B85421
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-374 <STO>
A:Cross-references: GB:NC_001268; NID:g7270518; PIDN:CAB80283.1; GSPDB:GN00140
C:Genetics:
A:Gene: AT4g35670
A:Map position: 4
C:Superfamily: polygalacturonase

Query Match      65.6%; Score 42; DB 2; Length 374;
Best Local Similarity 40.0%; Pred. No. 13;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 1 WYDPLTKLM 10
| | | | | : |
| | | | | : |

```

Db 91 WSDPISRMWI 100

## RESULT 9

T04672

polylacturonase homolog F8D20.180 - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C&gt;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 03-Nov-2000

C:Accession: T04672

R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Jesse, T.; Heijnen, L.; Vos, P.; Mewes,

submitted to the Protein Sequence Database, July 1998

A:Reference number: Z15381

A:Accession: T04672

A:Molecule type: DNA

A:Residues: 1-374 &lt;BEV&gt;

A:Cross-references: EMBL:AL031135

A:Experimental source: cultivar Columbia; BAC clone F8D20

C:Genetics:

A:Map position: 4

A:Note: intron positions not resolved

A:Note: F8D20.180

C:Superfamily: polylacturonase

Query Match 65.6%; Score 42; DB 2; Length 374;

Best Local Similarity 40.0%; Pred. No. 13;

Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WYDPLTKML 10

Db 91 WSDPISRMWI 100

## RESULT 10

T09371

hypothetical protein F23K16.180 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C&gt;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 14-Jul-2003

C:Accession: T09371

R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X

submitted to the Protein Sequence Database, June 1999

A:Reference number: Z16552

A:Accession: T09371

A:Molecule type: DNA

A:Residues: 1-392 &lt;BEV&gt;

A:Cross-references: EMBL:AL078620; GSPDB:GN00062; ATSP:F23K16.180

A:Experimental source: cultivar Columbia; BAC clone F23K16

C:Genetics:

A:Gene: ATSP:F23K16.180

A:Map position: 4

C:Superfamily: conserved hypothetical protein containing F-box and Kelch domains

Query Match 65.6%; Score 42; DB 2; Length 392;

Best Local Similarity 55.6%; Pred. No. 14;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WYDPLTKML 9

Db 297 WYDPMARLM 305

## RESULT 11

F82138

GSDP family protein VC1934 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C:Species: Vibrio cholerae

C&gt;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001

C:Accession: F82138

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;

charlson, D.; Ermojaeva, M.D.; Vamathavan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F

1, R.R.; Metalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen vibrio cholerae.

A:Reference number: A62035; MUID:20406833; PMID:10952301

A:Accession: F82138

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-655 &lt;HEI&gt;

A:Cross-references: GB:AE004269; GB:AE003852; NID:G9656466; PIDN:AAF95082.1; GSPDB:GN001

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC1934

A:Map position: 1

Query Match 64.1%; Score 41; DB 2; Length 655;

Best Local Similarity 75.0%; Pred. No. 35;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKL 8

Db 213 WMDPLTRL 220

## RESULT 12

H83315

hypothetical protein PA2635 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C&gt;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C:Accession: H83315

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yuan, X.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapid, K.; Lim,

Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho-

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: H83315

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-672 &lt;STD&gt;

A:Cross-references: GB:AE004692; GB:AE004091; NID:G9948701; PIDN:AA006023.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA2635

C:Superfamily: Campylobacter jejuni hypothetical protein Cj0145

Query Match 64.1%; Score 41; DB 2; Length 672;

Best Local Similarity 50.0%; Pred. No. 36;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WYDPLTKML 10

Db 566 WFDPEGRIMI 575

## RESULT 13

S16442

MIP protein - mouse

C:Species: Mus musculus (house mouse)

C&gt;Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 05-Nov-1999

C:Accession: S16442; S16443; S19092

R:Chang-Yeh, A.; Mold, D.E.; Huang, R.C.C.

Nucleic Acids Res. 19, 3667-3672, 1991

A:Title: Identification of a novel murine IAD-promoted placenta-expressed gene.

A:Reference number: S16442; MUID:91305114; PMID:1906605

A:Accession: S16442

A:Molecule type: mRNA

A:Residues: 1-202 &lt;CHA&gt;

A:Cross-references: EMBL:X58523; NID:G52733; PIDN:CAA41413.1; PID:G52734

A:Note: the authors translated the codon GCT for residue 20 as Gln, TCA for residue 21 a-

A:Accession: S16443

A:Molecule type: DNA

A:Residues: 1-41 &lt;CHA1&gt;

A:Cross-references: EMBL:X58524

R:Chang-Yeh, A.

submitted to the EMBL Data Library, March 1991

A:Reference number: S19092

A:Accession: S19092

A:Molecule type: DNA

A:Residues: 1-25, 'AVDMRYVCATGQSM' <CH2>  
A:Cross-references: EMBL:X58524; NID:g55731; PIDN:CAA414.1; PID:g55732  
A>Note: the difference at the carboxyl end is due to a frameshift error

Query Match 62.5%; Score 40; DB 2; Length 202;  
Best Local Similarity 75.0%; Pred. No. 15;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9  
|||:|  
Db 9 YDPLTKLM 16

## RESULT 14

A43586  
hypothetical protein 1 - Salmonella dublin plasmid PSD12

C:Species: Salmonella dublin

C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 08-Oct-1999

C:Accession: A43586

R:Krause, M.; Harwood, J.; Flierer, J.; Guiney, D.

Infect. Immun. 59, 1860-1863, 1991

A:Title: Genetic analysis of homology between the virulence plasmids of Salmonella dublin

A:Reference number: A43586; MUID:91209947; PMID:1840573

A:Accession: A43586

A:Molecule type: DNA

A:Residues: 1-345 <KRA>

A:Cross-references: GB:M58505; NID:g154215; PIDN:AA27173.1; PID:g154216

C:Genetics:

A:Genome: plasmid

Query Match 62.5%; Score 40; DB 2; Length 345;  
Best Local Similarity 50.0%; Pred. No. 27;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 10  
|:|:|  
Db 292 WYDPLTKLM 301

## RESULT 15

T47407

hypothetical protein F23N14.90 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 14-Jul-2003

C:Accession: T47407

R:Blocker, H.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.; Quettler, F.; Salanoub

submitted to the Protein Sequence database, March 2000

A:Reference number: Z24465

A:Accession: T47407

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-378 <BLO>

A:Cross-references: EMBL:AL138638

A:Experimental source: cultivar Columbia; BAC clone F23N14

C:Genetics:

A:Map position: 3

A>Note: F23N14.90

C:Superfamily: conserved hypothetical protein containing F-box and Kelch domains

Query Match 62.5%; Score 40; DB 2; Length 378;  
Best Local Similarity 66.7%; Pred. No. 29;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9  
|||:|  
Db 280 WYDPLTKLM 288

## RESULT 16

B87353  
hypothetical protein CC0837 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001

C:Accession: B87353

R:Nierman, W.C.; Feldlyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: B87353

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-519 <STO>

A:Cross-references: GB:AE05673; NID:g13422090; PIDN:AAK22822.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC0837

Query Match 62.5%; Score 40; DB 2; Length 519;  
Best Local Similarity 66.7%; Pred. No. 41;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9  
|||:|  
Db 414 WYDPLTKLM 422

## RESULT 17

S49622  
crk protein - Rhodobacter sphaeroides

C:Species: Rhodobacter sphaeroides

C:Date: 05-Mar-1995 #sequence\_revision 12-May-1995 #text\_change 04-Sep-1998

C:Accession: S49622

R:Lang, H.P.; Cogdell, R.J.; Takachi, S.; Hunter, C.N.

submitted to the EMBL Data Library, November 1994

A:Description: The complete DNA sequence, specific TMS insertion map and gene assignment

A:Reference number: S49619

A:Accession: S49622

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-157 <LAN>

A:Cross-references: EMBL:X82458; NID:g575405; PID:g575409

C:Genetics:

A:Gene: crk

C:Superfamily: tryptophan-rich sensory protein

Query Match 60.9%; Score 39; DB 2; Length 157;  
Best Local Similarity 66.7%; Pred. No. 17;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9  
|||:|  
Db 30 WYDPLTKLM 38

## RESULT 18

A57438  
tryptophan-rich sensory protein [similarity] - Rhodobacter sphaeroides (strain 2.4.1)

C:Species: Rhodobacter sphaeroides

C:Date: 26-Jan-1996 #sequence\_revision 26-Jan-1996 #text\_change 28-Jul-2000

C:Accession: A57438; T50747

R:Yeliseev, A.A.; Kaplan, S.

J. Biol. Chem. 270, 21167-21175, 1995

A:Title: A sensory transducer homologous to the mammalian peripheral-type benzodiazepine

A:Reference number: A57438; MUID:95403350; PMID:7673149

A:Accession: A57438

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-158 <YEL>

R:Choudhary, M.; Kaplan, S.

Nucleic Acids Res. 28, 862-867, 2000

A:Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides 2.

A:Reference number: Z25222; MUID:20115911; PMID:10648776

A:Accession: T50747

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A/Residues: 1-158 <CHO>  
A/Cross-references: EMBL:AF195122; PIDN:AAF24291.1  
A/Experimental source: strain 2.4.1  
C/Genetics:  
A/Gene: tspo  
C/Function:  
A/Description: tspo negatively regulates the activity of coproporphyrinogen III oxidase  
A/Note: tspo is supposed to cause the accumulation of a biosynthetic intermediate that is  
C/Superfamily: tryptophan-rich sensory protein  
C/Keywords: carotenoid biosynthesis

Query Match 60.9%; Score 39; DB 2; Length 158;  
Best Local Similarity 58.3%; Pred. No. 18;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYD-PLTKML 9  
DB 30 WYDNLNKPW 38

RESULT 19  
F64725  
Probable NAD(P)H oxidoreductase (quinone) (EC 1.6.99.2) yabF - Escherichia coli (strain  
C/Species: Escherichia coli  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 03-Jun-2002  
C/Accession: F64725; S40567  
R/Baltner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
.A.; Rose, D.U.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A/Title: The complete genome sequence of Escherichia coli K-12.  
A/Reference number: A64720; PMID:97426617; PMID:9278503  
A/Accession: F64725  
A/Status: nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-176 <BLAT>  
A/Cross-references: GB:AE000115; GB:U00096; NID:G1786230; PIDN:AACT73157.1; PID:G1786231;  
A/Experimental source: strain K-12, substrain MG1655  
R/Yuta, T.; Mori, H.; Nagai, H.; Nagata, T.; Ishihama, A.; Fujita, N.; Isono, K.; Mizobu  
submitted to the EMBL Data Library, December 1992  
A/Description: Systematic sequencing of the Escherichia coli genome: analysis of the 0-2  
A/Reference number: S40531  
A/Accession: S40567  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-78, 'N', 80-122, 'G', 124-176 <YUR>  
A/Cross-references: EMBL:D10483; NID:G216434; PIDN:BA01322.1; PID:G216471  
C/Genetics:  
A/Gene: yabF  
C/Superfamily: NAD(P)H dehydrogenase (quinone) 2  
C/Keywords: flavoprotein; NAD; oxidoreductase

Query Match 60.9%; Score 39; DB 1; Length 176;  
Best Local Similarity 58.3%; Pred. No. 20;  
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 WYD-PLTKML 10  
DB 67 WYSIPLKLMI 78

RESULT 20  
A85486  
Probable NAD(P)H oxidoreductase yabF [imported] - Escherichia coli (strain O157:H7, sub  
C/Species: Escherichia coli  
C/Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 17-May-2002  
C/Accession: A85486  
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glanier, J.D.; Rose, D.U.; Mayhew  
iller, U.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dinalanca, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A/Reference number: A85480; MUID:21074935; PMID:11206551  
A/Accession: A85486

A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-176 <STO>  
A/Cross-references: GB:AE005174; NID:G12512736; PIDN:AA654349.1; GSPDB:GN00145; UWGP:Z00  
A/Experimental source: strain O157:H7, substrain EDL933  
C/Genetics:  
A/Gene: yabF  
C/Superfamily: NAD(P)H dehydrogenase (quinone) 2

Query Match 60.9%; Score 39; DB 2; Length 176;  
Best Local Similarity 58.3%; Pred. No. 20;  
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 WYD-PLTKML 10  
DB 67 WYSIPLKLMI 78

RESULT 21  
A90635  
Probable NAD(P)H oxidoreductase EC0049 [imported] - Escherichia coli (strain O157:H7, s  
C/Species: Escherichia coli  
C/Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 17-May-2002  
C/Accession: A90635  
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gawara, N.; Yasunaga, T.; Kuahara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno  
A/Reference number: A99629; MUID:21156231; PMID:11258796  
A/Accession: A90635  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-176 <HAY>  
A/Cross-references: GB:BA000007; PIDN:BA03472.1; PID:G13359505; GSPDB:GN00154  
A/Experimental source: strain O157:H7, substrain RIMD 050952  
C/Genetics:  
A/Gene: EC0049  
C/Superfamily: NAD(P)H dehydrogenase (quinone) 2

Query Match 60.9%; Score 39; DB 2; Length 176;  
Best Local Similarity 58.3%; Pred. No. 20;  
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 WYD-PLTKML 10  
DB 67 WYSIPLKLMI 78

RESULT 22  
A10512  
Probable NAD(P)H oxidoreductase STY0100 [imported] - Salmonella enterica subsp. enterica  
C/Species: Salmonella enterica subsp. enterica serovar Typh  
A/Note: this species has also been called Salmonella typh  
C/Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C/Accession: A10512  
R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
, S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
A/Reference number: AB0502; MUID:21534947; PMID:11677608  
A/Accession: A10512  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-176 <PAR>  
A/Cross-references: GB:AL513382; PIDN:CAD01241.1; PID:G16501370; GSPDB:GN00176  
C/Genetics:  
A/Gene: STY0100  
C/Superfamily: NAD(P)H dehydrogenase (quinone) 2

Query Match 60.9%; Score 39; DB 2; Length 176;  
Best Local Similarity 58.3%; Pred. No. 20;

Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;  
QY 1 WYD--PLTKML 10  
|||  
Db 67 WYVPLTKMLW 78

## RESULT 23

WMLJSL  
bel-1 protein - simian foamy virus (type 1)

C:Species: simian foamy virus  
C:Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 16-Jul-1999  
C:Accession: B39924  
R:Merz, A.; Shaw, K.E.S.; Pratt-Lowe, E.; Barry, P.A.; Luciw, P.A.  
J:Virol. 65, 2903-2909, 1991  
A:Title: Identification of the simian foamy virus transcriptional transactivator gene (T  
A:Reference number: A39924; MUID:91237804; PMID:1851862  
A:Accession: B39924  
A:Molecule type: DNA  
A:Residues: 1-308 <MER>  
A:Cross-references: GB:M74039; NID:G334878; PID:AAA47802.1; PID:G454845  
C:Comment: This protein is a transcriptional transactivator.  
C:Genetics:  
A:Gene: bel-1; taf  
C:Superfamily: foamy virus bel-1 protein  
C:Keywords: transcription regulation

Query Match 60.9%; Score 39; DB 1; Length 308;  
Best Local Similarity 66.7%; Pred. No. 35;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YDPLTKML 10  
|||  
Db 155 YDPEELMW 163

## RESULT 24

S18740  
bell protein - simian foamy virus (fragment)

C:Species: simian foamy virus  
C:Date: 19-Mar-1997 #sequence\_revision 24-Jul-1997 #text\_change 31-Oct-1997  
C:Accession: S18740  
R:Kupiec, J.J.; Kay, A.; Hayat, M.; Ravier, R.; Perles, J.; Galibert, F.  
Gene 101, 185-194, 1991  
A:Title: Sequence analysis of the simian foamy virus type 1 genome.  
A:Reference number: S18737; MUID:91276270; PMID:1647358  
A:Accession: S18740  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-311 <KUP>  
A:Cross-references: EMBL:X54482  
C:Superfamily: foamy virus bel-1 protein

Query Match 60.9%; Score 39; DB 2; Length 311;  
Best Local Similarity 66.7%; Pred. No. 36;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YDPLTKML 10  
|||  
Db 158 YDPEELMW 166

## RESULT 25

S42424  
hypothetical protein Y - Mycobacterium smegmatis

C:Species: Mycobacterium smegmatis  
C:Date: 07-May-1998 #sequence\_revision 15-May-1998 #text\_change 22-Oct-1999  
C:Accession: S42424; S31804  
R:Citrillo, J.D.; Weisprod, T.R.; Pascopella, L.; Bloom, B.R.; Jacobs Jr., W.R.  
Mol. Microbiol. 11, 629-639, 1994  
A:Title: Isolation and characterization of the aspartokinase and aspartate semialdehyde  
A:Reference number: S42421; MUID:94254720; PMID:7910936  
A:Accession: S42424

A:Molecule type: DNA  
A:Residues: 1-333 <CTR>  
A:Cross-references: EMBL:Z17372; NID:G44506; PID:CA78987.1; PID:G581353  
A:Note: the authors translated the initiation codon GTG for residue 1 as Val  
C:Genetics:  
A:Start codon: GTG

Query Match 60.9%; Score 39; DB 2; Length 333;  
Best Local Similarity 66.7%; Pred. No. 38;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9  
|||  
Db 209 WGDPAALW 217

## RESULT 26

T48319  
hypothetical protein F15A17.10 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 21-Jul-2003  
C:Accession: T48319  
R:Bevan, M.; Terry, N.; Ardiles, W.; Buyschaert, C.; Dasseville, R.; De Clerck, R.; De  
ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.  
submitted to the Protein Sequence Database, April 2000  
A:Reference number: Z24491  
A:Accession: T48319  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-335 <BEV>  
A:Cross-references: EMBL:AL163002  
A:Experimental source: cultivar Columbia; BAC clone F15A17  
C:Genetics:  
A:Map position: 5  
A:Note: F15A17.10  
C:Superfamily: conserved hypothetical protein containing F-box and Kelch domains

Query Match 60.9%; Score 39; DB 2; Length 335;  
Best Local Similarity 66.7%; Pred. No. 39;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKML 10  
|||  
Db 176 YDPTTQTLW 184

## RESULT 27

T08577  
hypothetical protein T22F8.190 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 14-Jul-2003  
C:Accession: T08577  
R:Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; May  
submitted to the Protein Sequence Database, May 1999  
A:Reference number: Z16442  
A:Accession: T08577  
A:Molecule type: DNA  
A:Residues: 1-365 <BEV>  
A:Cross-references: EMBL:AL050351; GSPDB:GN00062; ATSP:T22F8.190  
A:Experimental source: cultivar Columbia; BAC clone T22F8  
C:Genetics:  
A:Gene: ATSP:T22F8.190  
A:Map position: 4  
C:Superfamily: conserved hypothetical protein containing F-box and Kelch domains

Query Match 60.9%; Score 39; DB 2; Length 365;  
Best Local Similarity 55.6%; Pred. No. 42;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9  
|||  
Db 272 WYDSCKIMW 280



## RESULT 28

hypothetical protein C53A5.11 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C:Accession: T20170

R:Mortimore, B.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19232

A:Accession: T20170

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-430 <NT>

A:Cross-references: EMBL:Z81486; PIDN:CA030991.1; GSPDB:GN00023; CESP:C53A5.11

A:Experimental source: clone C53A5

C:Genetics:

A:Gene: CESP:C53A5.11

A:Map position: 5

A:Introns: 30/3; 52/3; 170/1; 240/3; 309/1

Query Match 60.9%; Score 39; DB 2; Length 430;

Best Local Similarity 75.0%; Pred. No. 50;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9

DB 372 YDPLTNTW 379

## RESULT 29

hypothetical protein C53A5.9 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C:Accession: T20168

R:Mortimore, B.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19232

A:Accession: T20168

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-480 <NT>

A:Cross-references: EMBL:Z81486; PIDN:CA030989.1; GSPDB:GN00023; CESP:C53A5.9

A:Experimental source: clone C53A5

C:Genetics:

A:Gene: CESP:C53A5.9

A:Map position: 5

A:Introns: 28/1; 59/3; 194/1; 264/3; 332/1

Query Match 60.9%; Score 39; DB 2; Length 480;

Best Local Similarity 75.0%; Pred. No. 56;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9

DB 396 YDPLTKTW 403

## RESULT 30

1-lactate permease - Helicobacter pylori (strain J99)

C:Species: Helicobacter pylori

A:Variety: strain J99

C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 29-Sep-1999

C:Accession: D71969

R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;

Nature 397, 176-180, 1999

A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path

A:Reference number: A71800; MUID:99120557; PMID:9923682

A:Accession: D71969

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-551 <ARN>

A:Cross-references: GB:AE001452; GB:AE001439; NID:g4154639; PIDN:AA05719.1; PID:g4154651

A:Experimental source: strain J99

C:Genetics:

A:Gene: lldp 2

C:Superfamily: L-lactate permease

Query Match 60.9%; Score 39; DB 2; Length 551;

Best Local Similarity 66.7%; Pred. No. 65;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKML 10

DB 8 YDPLGNITWL 16

## RESULT 31

1-lactate permease - Helicobacter pylori (strain 26695)

C:Species: Helicobacter pylori

C:Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 29-Sep-1999

C:Accession: E64537

R:Tomb, J.F.; White, O.; Kexlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen-

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.

Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Frazer, C.;

A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; MUID:97394467; PMID:9252185

A:Accession: E64537

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-551 <TOM>

A:Cross-references: GB:AE000535; GB:AE000511; NID:g2313217; PIDN:AA07209.1; PID:g2313222

C:Genetics:

A:Start codon: GTG

C:Superfamily: L-lactate permease

Query Match 60.9%; Score 39; DB 2; Length 551;

Best Local Similarity 66.7%; Pred. No. 65;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKML 10

DB 8 YDPLGNITWL 16

## RESULT 32

Probable integral membrane protein [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001

C:Accession: B66989

R:Coile, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hou-

R.; Davies, R.M.; Devlin, K.; Duttoy, S.; Feltwell, T.; Frazer, A.; Hamlin, N.; Holroyd,

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, W.; Skelton, J.; Squares, R.; Sq

A:Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A66909; MUID:21128732; PMID:11234002

A:Accession: B66989

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-983 <STD>

A:Cross-references: GB:AL450380; NID:g13092818; PIDN:CA030153.1; GSPDB:GN00147

C:Genetics:

A:Gene: ML0644

Query Match 60.9%; Score 39; DB 2; Length 983;

Best Local Similarity 55.6%; Pred. No. 1.2e+02;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YDPLTKLWL 10  
| | | | |  
Db 666 YDPLTKLWV 674

## RESULT 33

T37218  
hypothetical protein SC2H4.02 - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C:Accession: T37218  
R:Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, September 1998  
A:Reference number: Z21615  
A:Accession: T37218  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-2183 <OLI>  
A:Cross-references: EMBL:AL031514; PIDN:CMA20596.1; GSPDB:GN00070; SCOEDB:SC2H4.02  
A:Experimental source: strain A3(2)  
C:Genetics:  
A:Gene: SCOEDB:SC2H4.02

Query Match 60.9%; Score 39; DB 2; Length 2183;  
Best Local Similarity 66.7%; Pred. No. 2.8e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLW 9  
| | | | |  
Db 1942 WTQPLTKW 1950

## RESULT 34

B83990  
hypothetical protein BH2722 [imported] - Bacillus halodurans (strain C-125)  
C:Species: Bacillus halodurans  
C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
C:Accession: B83990  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A:Reference number: A83650; MUID:20512582; PMID:11058132  
A:Accession: B83990  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-190 <STO>  
A:Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAH06441.1; GSPDB:GNOC  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: BH2722

Query Match 59.4%; Score 38; DB 2; Length 190;  
Best Local Similarity 70.0%; Pred. No. 32;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLW 10  
| | | | |  
Db 146 WTVDLTKLW 155

## RESULT 35

G69057  
hypothetical protein MTH1433 - Methanobacterium thermoautotrophicum (strain Delta H)  
C:Species: Methanobacterium thermoautotrophicum  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 22-Oct-1999  
C:Accession: G69057  
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;  
Qu, D.; Spadafora, R.; Vcalate, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jivani, N.;  
Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997  
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func  
A:Reference number: A69000; MUID:98037514; PMID:9371463  
A:Accession: G69057

A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-206 <MTH>  
A:Cross-references: GB:AE000905; GB:AE000666; NID:g2622541; PIDN:AAB85908.1; PID:g2622541  
A:Experimental source: strain Delta H  
C:Genetics:  
A:Gene: MTH1433

Query Match 59.4%; Score 38; DB 2; Length 206;  
Best Local Similarity 75.0%; Pred. No. 34;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKLW 9  
| | | | |  
Db 106 YDPLTKRW 113

## RESULT 36

T32202  
hypothetical protein T02B11.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
C:Accession: T32202  
R:Goela, D.  
submitted to the EMBL Data Library, September 1997  
A:Description: The sequence of C. elegans cosmid T02B11.  
A:Reference number: Z21135  
A:Accession: T32202  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-295 <GOE>  
A:Cross-references: EMBL:AF022979; PIDN:AAB69903.1; GSPDB:GN00023; CESP:T02B11.1  
A:Experimental source: strain Bristol N2; clone T02B11  
C:Genetics:  
A:Gene: CESP:T02B11.1  
A:Map position: 5  
A:Inserts: 161/3; 250/3

Query Match 59.4%; Score 38; DB 2; Length 295;  
Best Local Similarity 85.7%; Pred. No. 50;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PLTKLW 10  
| | | | |  
Db 3 PLTKLW 9

## RESULT 37

T50966  
hypothetical protein B24P7.210 [imported] - Neurospora crassa  
C:Species: Neurospora crassa  
C:Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 21-Jul-2000  
C:Accession: T50966  
R:Schulte, U.; Aign, V.; Heiseisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,  
submitted to the Protein Sequence Database, July 2000  
A:Reference number: Z25286  
A:Accession: T50966  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-321 <SCH>  
A:Cross-references: EMBL:AL389890; GSPDB:GN00116; NCSP:B24P7.210  
A:Experimental source: BAC clone B24P7; strain OR74A  
C:Genetics:  
A:Gene: NCSP:B24P7.210  
A:Map position: 6  
A:Inserts: 208/3

Query Match 59.4%; Score 38; DB 2; Length 321;  
Best Local Similarity 55.6%; Pred. No. 55;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLW 9  
| | | | |

Db 114 WYKXIAKLM 122

RESULT 38  
B83298

conserved hypothetical protein PA2771 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Accession: B83298  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Species: Pseudomonas aeruginosa  
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lathig, K.; Lim,  
; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A:Reference number: AB2950; MUID:2043737; PMID:10954043  
A:Accession: B83298  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-341 <STO>  
A:Cross-references: GB:AE004705; GB:AE004091; NID:g9948851; PIDN:AAG06159.1; GSPDB:GN001  
A:Experimental source: strain PA01  
C:Genetics:

Query Match 59.4%; Score 38; DB 2; Length 341;  
Best Local Similarity 85.7%; Pred. No. 58;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 DPLTKLM 9  
Db 184 DPLTKLM 190RESULT 39  
A13513

ATPase virB11 homolog BMEI10035 [imported] - Brucella melitensis (strain 16M)  
C:Species: Brucella melitensis  
C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 15-Feb-2002  
C:Accession: A13513  
R:DelVecchio, V.G.; Kapral, V.; Redkar, R.V.; Patra, G.; Mujer, C.; Ios, T.; Ivanova,  
; Mazur, M.; Goldsman, E.; Selkov, E.; Elizer, P.H.; Hagius, S.; O'Callaghan, D.; Leles  
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitens  
A:Reference number: AD3252; PMID:11756688  
A:Accession: A13513  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-361 <KUR>  
A:Cross-references: GB:AE008918; PIDN:AAL53276.1; PID:g17984158; GSPDB:GN00191  
A:Experimental source: strain 16M  
C:Genetics:  
A:Gene: BMEI10035  
A:Map position: 11  
C:Superfamily: tumor-inducing plasmid pTIC58 virB11 protein

Query Match 59.4%; Score 38; DB 2; Length 361;  
Best Local Similarity 85.7%; Pred. No. 62;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYDPLTK 7  
Db 343 WYDPLTK 349RESULT 40  
T00683

hypothetical protein At2g44030 [imported] - Arabidopsis thaliana  
N:Alternate names: hypothetical protein F6E13.16  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 14-Jul-2003  
C:Accession: T00683; B84873  
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,  
submitted to the EMBL Data Library, June 1998

A:Description: Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence.  
A:Reference number: Z14180

A:Accession: T00683  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-380 <ROU>  
A:Cross-references: EMBL:AC004005; NID:g3212846; PID:g3212860  
A:Experimental source: cultivar Columbia  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shee, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: AB4420; MUID:20083487; PMID:10617197  
A:Accession: B84873  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-380 <STO>  
A:Cross-references: GB:AE002093; NID:g3212860; PIDN:AAC23411.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: F6E13.16; At2g44030  
A:Map position: 2  
C:Superfamily: conserved hypothetical protein containing F-box and Kelch domains

Query Match 59.4%; Score 38; DB 2; Length 380;  
Best Local Similarity 62.5%; Pred. No. 66;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9  
Db 192 YDPLTKLM 199RESULT 41  
AC2650

glucose-6-phosphate 1-dehydrogenase zwf [imported] - Agrobacterium tumefaciens (strain C)  
C:Species: Agrobacterium tumefaciens  
C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002  
C:Accession: AC2650  
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L  
erage, P.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McCell  
; Karp, G.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A:Reference number: AB2577; MUID:21608550; PMID:11743193  
A:Accession: AC2650  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-491 <KUR>  
A:Cross-references: GB:AE00688; PIDN:AAL41617.1; PID:g17738955; GSPDB:GN00186  
A:Experimental source: strain C58 (Dupont)  
C:Genetics:  
A:Gene: zwf  
A:Map position: circular chromosome  
C:Superfamily: glucose-6-phosphate dehydrogenase

Query Match 59.4%; Score 38; DB 2; Length 491;  
Best Local Similarity 55.6%; Pred. No. 86;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9  
Db 448 WYDPLTKLM 456RESULT 42  
B97432

glucose-6-phosphate 1-dehydrogenase (g6pd) [imported] - Agrobacterium tumefaciens (strain  
C:Species: Agrobacterium tumefaciens  
C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 18-Nov-2002  
C:Accession: B97432

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001  
A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*  
A;Reference number: A97459; MUID:21608551; PMID:11743194  
A;Accession: B97432  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-503 <KUR>  
A;Cross-references: GB:AE007869; PIDN:AAK86411.1; PID:g15155545; GSPDB:GN00169  
C;Genetics:  
A;Gene: AGR\_C\_1065  
A;Map position: circular chromosome  
C;Superfamily: glucose-6-phosphate dehydrogenase

Query Match 59.4%; Score 38; DB 2; Length 503;  
Best Local Similarity 55.6%; Pred. No. 88;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9  
DB 460 WIDPLIKSW 468

RESULT 43  
C71969  
L-lactate permease - *Helicobacter pylori* (strain J99)  
C;Species: *Helicobacter pylori*  
A;Variety: strain J99  
C;Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 29-Sep-1999  
C;Accession: C71969  
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Miller, S.D.; Jiang, Q.; Taylor, D.E.; Voris, G.F.; Nature 397, 176-180, 1999  
A>Title: Genomic sequence comparison of two unrelated isolates of the human gastric path  
A;Reference number: A71800; MUID:99120557; PMID:9923682  
A;Accession: C71969  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-549 <ARN>  
A;Cross-references: GB:AE001452; GB:AE001439; NID:g4154639; PIDN:AAD05718.1; PID:g415464  
A;Experimental source: strain J99  
C;Genetics:  
A;Gene: lldp\_1  
C;Superfamily: L-lactate permease

Query Match 59.4%; Score 38; DB 2; Length 549;  
Best Local Similarity 66.7%; Pred. No. 96;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLW 10  
DB 7 YDPLGH1WL 15

RESULT 44  
D64537  
L-lactate permease - *Helicobacter pylori* (strain 26695)  
C;Species: *Helicobacter pylori*  
C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 29-Sep-1999  
C;Accession: D64537  
R;Tomb, J.F.; White, O.; Kellavagge, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khatkhat, H.G.; Glodek, A.; McKenna, Nature 388, 539-547, 1997  
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A>Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.  
A;Reference number: A64520; MUID:97394467; PMID:9252185  
A;Accession: D64537  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-549 <TOM>  
A;Cross-references: GB:AE000535; GB:AE000511; NID:g2313217; PIDN:AAD07208.1; PID:g231322

C;Superfamily: L-lactate permease

Query Match 59.4%; Score 38; DB 2; Length 549;  
Best Local Similarity 66.7%; Pred. No. 96;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLW 10  
DB 7 YDPLGH1WL 15

RESULT 45  
F81423  
L-lactate permease Cj0076c [imported] - *Campylobacter jejuni* (strain NCTC 11168)  
C;Species: *Campylobacter jejuni*  
C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 03-Jun-2002  
C;Accession: F81423  
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Kelsey, J.M.; Churcher, C.; Basham, D.; Chilling, C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrall, Nature 403, 665-668, 2000  
A>Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hyp  
A;Reference number: A81250; MUID:20150912; PMID:10688204  
A;Accession: F81423  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-560 <PAR>  
A;Cross-references: GB:AL139074; GB:AL111168; NID:g6967505; PIDN:CAW72562.1; PID:g696757;  
A;Experimental source: serotype O2, strain NCTC 11168  
C;Genetics:  
A;Gene: lcp; Cj0076c  
C;Superfamily: L-lactate permease

Query Match 59.4%; Score 38; DB 2; Length 560;  
Best Local Similarity 55.6%; Pred. No. 98;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLW 10  
DB 11 YDPLSN1WL 19

RESULT 46  
F90485  
hypothetical protein SSO3039 [imported] - *Sulfolobus solfataricus*  
C;Species: *Sulfolobus solfataricus*  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 21-Jul-2003  
C;Accession: F90485  
R;Sne, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweyer, M.J.; Chan-I, J.; Jongs, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. submitted to Genbank, April 2001  
A;Description: *Sulfolobus solfataricus* complete genome.  
A;Reference number: A99139  
A;Accession: F90485  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-803 <KUR>  
A;Cross-references: GB:AE006641; NID:g13816440; PIDN:AAK43141.1; GSPDB:GN00155  
C;Genetics:  
A;Gene: SSO3039  
C;Superfamily: beta-glucosidase, GBA2 type

Query Match 59.4%; Score 38; DB 2; Length 803;  
Best Local Similarity 62.5%; Pred. No. 1.4e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 8  
DB 596 WYDPLSNL 603

RESULT 47  
T46253

hypothetical protein DKF2p761F17.1 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 04-Feb-2000  
C:Accession: T46253  
R:Ostenwelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, January 2000  
A:Reference number: 223031  
A:Accession: T46253  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-849 <AAA>  
A:Cross-references: EMBL:AL137500  
A:Experimental source: adult amygdala; clone DKF2p761F17.1  
C:Genetics:  
A:Note: DKF2p761F17.1

Query Match 59.4%; Score 38; DB 2; Length 849;  
Best Local Similarity 100.0%; Pred. No. 1.56+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YDPLTKL 8  
DB 491 YDPLTKL 497

RESULT 48  
T51593  
GTP-binding regulatory protein extra-large [validated] - Arabidopsis thaliana  
N:Alternate names: G-protein extra-large  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
C:Accession: T51593  
R:Lee, Y.R.; Asmann, S.M.  
Plant Mol. Biol. 40, 55-64, 1999  
A>Title: Arabidopsis thaliana 'extra-large GTP-binding protein' (AtXUG1): a new class of  
A:Reference number: 225403; MUID:99320868; PMID:10394945  
A:Accession: T51593  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-888 <LEE>  
A:Cross-references: EMBL:AF060941; PIDN:AAC19352.1  
A:Experimental source: cultivar Columbia  
C:Genetics:  
A:Gene: XUG1  
C:Function:  
A:Description: binds GTP with specificity [validated; MUID:99320868]

Query Match 59.4%; Score 38; DB 2; Length 888;  
Best Local Similarity 55.6%; Pred. No. 1.6e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKL 9  
DB 348 WYDPLTKL 356

RESULT 49  
T01135  
probable GTP-binding protein (extra large) [imported] - Arabidopsis thaliana  
N:Alternate names: hypothetical protein F26B6.11  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 02-Feb-2001  
C:Accession: T01135; A84625  
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,  
submitted to the EMBL Data Library, June 1998  
A:Description: Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence.  
A:Reference number: 214198  
A:Accession: T01135  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-901 <ROU>  
A:Cross-references: EMBL:AC003040; NID:G3242700; PID:G3242700  
A:Experimental source: cultivar Columbia

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Unayama, L.;  
eius, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J  
Nature 402, 761-768, 1999  
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: A84625  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-901 <STO>  
A:Cross-references: GB:AE02093; NID:G3242709; PIDN:AAC3761.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g23460; F26B6.11  
A:Map position: 2  
A:Introns: 358/3; 439/3; 502/3; 565/1; 646/3; 701/2

Query Match 59.4%; Score 38; DB 2; Length 901;  
Best Local Similarity 55.6%; Pred. No. 1.6e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKL 9  
DB 348 WYDPLTKL 356

RESULT 50  
S76592  
5-methyltetrahydrofolate-homocysteine S-methyltransferase (EC 2.1.1.13) [similarity] - S  
C:Species: Synchocystis sp.  
A:Variety: PCC 6803  
C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 03-Jun-2002  
C:Accession: S76592  
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;  
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
DNA Res. 3, 109-136, 1996  
A>Title: Sequence analysis of the genome of the unicellular cyanobacterium Synchocystis  
S.  
A:Reference number: S74322; MUID:97061201; PMID:8905231  
A:Accession: S76592  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1195 <KAN>  
A:Cross-references: EMBL:D64002; GB:AB001339; NID:G1001612; PIDN:BA10438.1; PID:G1001701  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C:Superfamily: cobalamin-dependent methionine synthase; cobalamin-binding homology  
F:Keywords: methyltransferase  
F:737/Binding site: methylcobalamin cobalt (His) (axial ligand) #status predicted

Query Match 59.4%; Score 38; DB 2; Length 1195;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YDPLTKL 8  
DB 611 YDPLTKL 617

RESULT 51  
T15881  
hypothetical protein D1044.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
C:Accession: T15881  
R:Pauley, A.  
submitted to the EMBL Data Library, June 1994  
A:Description: The sequence of C. elegans cosmid D1044.  
A:Reference number: 218423  
A:Accession: T15881  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1895 <PAU>  
A:Cross-references: EMBL:U00065; NID:G495681; PID:G495684; PIDN:AAA50735.1; CESP:D1044.3  
A:Experimental source: strain Bristol N2

## C:Genetics:

A:Gene: CESP:DL044.3  
A:Introns: 35/2; 63/2; 150/1; 191/3; 207/2; 405/3; 551/3; 629/1; 764/1; 933/1; 959/2; 10

Query Match  
Best Local Similarity 59.4%; Score 38; DB 2; Length 1895;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9  
||| |

Db 659 YDPLTKLM 666

## RESULT 52

T14271

Doc4 protein, stress-induced - mouse

N:Alternate names: odz protein homolog

C:Species: Mus musculus (house mouse)

C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999

C:Accession: T14271

R:Wang, X.Z.; Kuroda, M.; Sok, J.; Batchvarova, N.; Kimmel, R.; Chung, P.; Zinszner, H.;

EMBO J. 17, 3613-3630, 1998

A>Title: Identification of novel stress-induced genes downstream of chop.

A:Reference number: 217951; MUID:98315054; PMID:9649432

A:Accession: T14271

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-2825 <MAN>

A:Cross-references: EMBL:AF059485; NID:g3170614; PID:g3170615; PIDN:AAC31807.1

C:Genetics:

A:Gene: Doc4

Query Match  
Best Local Similarity 59.4%; Score 38; DB 2; Length 2825;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YDPLTKLM 8  
||| |

Db 2463 YDPLTKLM 2469

## RESULT 53

A70885  
Hypothetical protein Rv2794c - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000

C:Accession: A70885

R:COLE, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: A70885

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-227 <CO>

A:Cross-references: GB:AL008967; GB:AL123456; NID:g3261491; PIDN:CAA1589.1; PID:g262431

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: Rv2794c

Query Match  
Best Local Similarity 58.6%; Score 37.5; DB 2; Length 227;

Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 WYDPLTKLM 10  
||| |

Db 163 WF-PLTKRL 171

## RESULT 54

## E87102

Conserved hypothetical protein ML1547 [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C>Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001

C:Accession: E87102

R:COLE, S.T.; Eigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor

R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Felwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squ

A>Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A86909; MUID:21128732; PMID:11234002

A:Accession: E87102

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-227 <STO>

A:Cross-references: GB:AL450380; NID:g13093366; PIDN:CAC30498.1; GSPDB:GN00147

C:Genetics:

A:Gene: ML1547

Query Match  
Best Local Similarity 58.6%; Score 37.5; DB 2; Length 227;

Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 WYDPLTKLM 10  
||| |

Db 163 WF-PLTKRL 171

## RESULT 55

C40626  
dihydrodipicolinate synthase (EC 4.2.1.52) precursor [similarity] - Corynebacterium glut

N:Alternate names: L-2,3-dihydrodipicolinate synthetase

C:Species: Corynebacterium glutamicum

C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 17-Mar-2000

C:Accession: C40626; S12105

R:Plasbarro, A.; Malumbres, M.; Mateos, I.M.; Oguita, J.A.; Martin, J.F.

J. Bacteriol. 175, 2743-2749, 1993

A>Title: A cluster of three genes (dapA, orf2, and dapB) of Brevibacterium lactofermentum

ion.

A:Reference number: A40626; MUID:93239702; PMID:8478336

A:Accession: C40626

A:Molecule type: DNA

A:Residues: 1-301 <PIS>

A:Cross-references: GB:Z21502; GB:S59668; NID:g311767; PIDN:CAA79714.1; PID:g311770

A:Experimental source: ATCC 13639

A>Note: sequence extracted from NCBI backbone (NCBIN:130448, NCBIP:130451)

R:Bommaslie, S.; Oreglia, J.; Sicard, A.M.

Nucleic Acids Res. 18, 6421, 1990

A>Title: Nucleotide sequence of the dapA gene from Corynebacterium glutamicum.

A:Reference number: S12105; MUID:91057127; PMID:2129555

A:Accession: S12105

A:Molecule type: DNA

A:Residues: 1-265; 'S', 267-301 <BON>

A:Cross-references: EMBL:X53993; NID:g40490; PIDN:CAA37940.1; PID:g40491

A:Experimental source: AS019

C:Genetics:

A:Gene: dapA

A:Function: catalyzes the condensation of pyruvate and L-aspartate 4-semialdehyde to L

A:Pathway: diaminopimelate-lysine biosynthesis

A>Note: this enzyme may catalyze only the condensation of pyruvate and L-aspartate 4-sem

C:Superfamily: dihydrodipicolinate synthase

C:Keywords: carbon-oxygen lyase; diaminopimelate-lysine biosynthesis; hydro-lyase

F;173/Active site: Lys (covalent pyruvate-binding) #status Predicted

Query Match  
Best Local Similarity 58.6%; Score 37.5; DB 1; Length 301;

Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 1 WY--DPLTKLM 10  
||| |

Db 193 WYSGDDPLNLAWL 205

RESULT 56  
H87263  
hypothetical protein CC0121 [imported] - *Caulobacter crescentus*  
C:Species: *Caulobacter crescentus*  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001  
C:Accession: H87263  
R:Niemann, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laid, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Esmolaev, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of *Caulobacter crescentus*.  
A:Reference number: A87249; MUID:21173698; PMID:11259647  
A:Accession: H87263  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-151 <STO>  
A:Cross-references: GB:AE005673; NID:g13421228; PIDN:AK22108.1; GSPDB:GN00148  
C:Genetics:  
A:Gene: CC0121

Query Match 57.8%; Score 37; DB 2; Length 151;  
Best Local Similarity 50.0%; Pred. No. 37;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
| | | | |  
| | | | |  
Db 37 WRDPVREAWL 46

RESULT 57  
B5833  
partial probable sensor kinase Z3235 [imported] - *Escherichia coli* (strain O157:H7, subS  
C:Species: *Escherichia coli*  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C:Accession: B5833  
R:Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew  
Hiller, L.; Grobeck, E.J.; Davis, N.W.; Lm, A.; Dimalanta, E.; Potamousts, K.; Apodaca,  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: B5833  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-177 <STO>  
A:Cross-references: GB:AE005174; NID:g12516269; PIDN:AG57129.1; GSPDB:GN00145; UWGP:Z32  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: Z3235

Query Match 57.8%; Score 37; DB 2; Length 177;  
Best Local Similarity 58.3%; Pred. No. 44;  
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 WYDPLTKLWL 10  
| | | | |  
| | | | |  
Db 114 WYNPLONLADWL 125

RESULT 58  
B90988  
partial probable sensor kinase EC62874 [similarity] - *Escherichia coli* (strain O157:H7,  
C:Species: *Escherichia coli*  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 02-Nov-2001  
C:Accession: B90988  
R:Havash, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
Gasanara, N.; Yasunaga, T.; Kihara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and geno  
A:Reference number: A9629; MUID:21156231; PMID:11258796  
A:Accession: B90988

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-177 <HAY>  
A:Cross-references: GB:BA000007; PIDN:BA36297.1; PID:g13362343; GSPDB:GN00154  
A:Experimental source: strain O157:H7, substrain RMD 0509952  
C:Genetics:  
A:Gene: EC62874

Query Match 57.8%; Score 37; DB 2; Length 177;  
Best Local Similarity 58.3%; Pred. No. 44;  
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 WYDPLTKLWL 10  
| | | | |  
| | | | |  
Db 114 WYNPLONLADWL 125

RESULT 59  
AB0665  
conserved hypothetical protein STY1429 [imported] - *Salmonella enterica* subsp. *enterica*  
C:Species: *Salmonella enterica* subsp. *enterica* serovar Typh  
A:Note: this species has also been called *Salmonella typhi*  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C:Accession: AB0665  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
th, T.; Comerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov  
A:Reference number: AB0502; MUID:21534947; PMID:11677608  
A:Accession: AB0665  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-266 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CA001691.1; PID:g16502542; GSPDB:GN00176  
C:Genetics:  
A:Gene: STY1429

Query Match 57.8%; Score 37; DB 2; Length 266;  
Best Local Similarity 50.0%; Pred. No. 67;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
| | | | |  
| | | | |  
Db 110 WHPAEKIWL 119

RESULT 60  
B69751  
conserved hypothetical protein ybgG - *Bacillus subtilis*  
C:Species: *Bacillus subtilis*  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 15-Oct-1999  
C:Accession: B69751  
R:Kunst, F.; Ogasawara, N.; Mooser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertsch  
C.; Bron, S.; Brouillet, S.; Brusch, G.V.; Caldwell, B.; Capiano, V.; Carter, N.M.; Cho  
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler  
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinis  
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
Y.M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetalle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,  
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowaka, A.; Seror  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetre, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winers, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K  
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: B69751  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA

A:Residues: 1-315 <KTN>  
A:Cross-references: GB:299105; GB:AL009126; NID:g2632457; PIDN:CAB12035.1; PID:e1182193;  
A:Experimental source: Strain 168  
C:Genetics:  
A:Gene: ybgG

Query Match 57.8%; Score 37; DB 2; Length 315;  
Best Local Similarity 75.0%; Pred. No. 80;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 WYDPLTKLM 9  
DB 260 WYDPLTKLM 267

RESULT 61  
T15395  
hypothetical protein C03F11.2 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
C:Accession: T15395  
R:Bentley, D.

submitted to the EMBL Data Library, October 1995  
A:Description: The sequence of C. elegans cosmid C03F11.  
A:Reference number: Z18342

A:Accession: T15395  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-316 <BEN>

A:Cross-references: EMBL:U39744; NID:g1049465; PID:g1049467; PIDN:AAA80440.1; CESP:C03F11  
C:Genetics:  
A:Gene: CESP:C03F11.2  
A:introns: 90/3; 133/2; 171/1; 227/1; 262/1; 309/2

Query Match 57.8%; Score 37; DB 2; Length 316;  
Best Local Similarity 66.7%; Pred. No. 80;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9  
DB 301 WYDPLTKLM 309

RESULT 62

S67858  
guni protein - *Xanthomonas campestris*  
C:Species: *Xanthomonas campestris*

C:Date: 24-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 04-Mar-2000  
C:Accession: S67858  
R:Pollock, T.J.

submitted to the EMBL Data Library, March 1995  
A:Reference number: S67858

A:Accession: S67858

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-349 <POL>

A:Cross-references: EMBL:U22511; NID:g1172090; PIDN:AAA86377.1; PID:g733150

C:Genetics:

A:Gene: guni

C:Superfamily: *Xanthomonas campestris* guni protein

Query Match 57.8%; Score 37; DB 2; Length 349;  
Best Local Similarity 50.0%; Pred. No. 89;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 10  
DB 125 WYDPLTKLM 134

RESULT 63

E82902  
citrate-dependent iron transport, membrane-bound protein UUS57 [imported] - *Ureaplasma*

C:Species: *Ureaplasma urealyticum*

C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000

C:Accession: E82902

R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Casseil, G.H.

submitted to GenBank, February 2000

A:Description: The complete sequence of *Ureaplasma urealyticum*: Alternate views of a min

A:Reference number: A82870

A:Accession: E82902

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-356 <GLA>

A:Cross-references: GB:AE002132; GB:AF222894; NID:g6899327; PIDN:AAF30766.1; GSPDB:GN001

A:Experimental source: serovar 3, biovar 1

C:Genetics:

A:Gene: fecD; UUS57

A:Genetic code: SGC3

Query Match 57.8%; Score 37; DB 2; Length 356;  
Best Local Similarity 50.0%; Pred. No. 91;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 10  
DB 91 WYDPLTKLM 100

RESULT 64

A95326  
probable AtcC [imported] - *Sinorhizobium meliloti* (strain 1021) magaplasmid pSymA

C:Species: *Sinorhizobium meliloti*

C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001

C:Accession: A95326

R:Barrett, M.O.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse

; Kalmann, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surryck, R.; Wells, D.H.; Yeh, K.C.;

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A:Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti*

A:Reference number: A95326; MUID:21396509; PMID:11481432

A:Accession: A95326

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-357 <KUR>

A:Cross-references: GB:AE006469; PIDN:AAK65171.1; PID:g14523615; GSPDB:GN00165

A:Experimental source: strain 1021, megaplasmid pSymA

R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalmann, S.; Keating, D.H.; Kiss, E.; Komp, C.; LeLaure,

hebaule, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.

A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.

A:Reference number: A96039; MUID:21368234; PMID:11474104

A:Contents: annotation

C:Genetics:

A:Gene: Sma0950

A:Genome: plasmid

Query Match 57.8%; Score 37; DB 2; Length 357;  
Best Local Similarity 71.4%; Pred. No. 91;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYDPLTK 7  
DB 52 WYDPLTK 58

RESULT 65

BUBX2  
MAK32 protein - yeast (*Saccharomyces cerevisiae*)

N:Alternate names: protein YCR019w

C:Species: *Saccharomyces cerevisiae*

C:Date: 30-Jun-1991 #sequence\_revision 30-Sep-1993 #text\_change 16-Jun-2000

C:Accession: S19429; S07695

R:Feldmann, H.; Mannhaupt, G.; Vetter, I.



submitted to the Protein Sequence Database, March 1992  
A:Reference number: S19429  
A:Accession: S19429  
A:Molecule type: DNA  
A:Residues: 1-363 <FEU>  
A:Cross-references: EMBL:X59720; NID:g1907116; PIDN:CAA42310.1; PID:g1907162; GSPDB:GN001  
R:Toh-e, A.; Sabaishi, Y.  
Yeast 1, 159-171, 1985  
A>Title: The PET1 locus of *Saccharomyces cerevisiae*: a complex locus containing multiple  
A:Reference number: S07692; MUID:89131254; PMID:3916862  
A:Accession: S07695  
A:Molecule type: DNA  
A:Residues: 1-14, '1', 15-81, 83-282, 'S', 284-363 <TOH>  
C:Genetics:  
A:Gene: SGD:MAK32, MIPS:YCR019W  
A:Cross-references: SGD:S0000612; MIPS:YCR019W  
A:Map position: 3R  
C:Superfamily: MAK32 protein

Query Match 57.8%; Score 37; DB 1; Length 363;  
Best Local Similarity 62.5%; Pred. No. 93;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLW 9  
|||: |||  
Db 325 YDPLTKW 332

RESULT 66  
S42003  
sterol 24-C-methyltransferase (EC 2.1.1.41) - yeast (*Saccharomyces cerevisiae*)  
N:Alternate names: PDR4-region bioc homolog; protein YM571.10c; protein YML008c  
C:Species: *Saccharomyces cerevisiae*  
C>Date: 03-Feb-1994 #sequence\_revision 27-Jan-1995 #text\_change 03-Jun-2002  
C:Accession: S42003; PEO402; S55111; S17001; S35982  
R:Hardwick, K.G.; Pelham, H.R.B.  
Yeast 10, 265-269, 1994  
A>Title: SMD6 is identical to ERG6, and encodes a putative methyltransferase required for  
A:Reference number: S42003; MUID:94262330; PMID:8203167  
A:Accession: S42003  
A:Molecule type: DNA  
A:Residues: 1-383 <HAR>  
A:Cross-references: EMBL:X74249; NID:9396514; PIDN:CAA52308.1; PID:9396515  
A>Note: the authors translated the codon ACT for residue 322 as Ala  
R:Hussain, M.; Lenard, J.  
Gene 101, 149-152, 1991  
A>Title: Characterization of PDR4, a *Saccharomyces cerevisiae* gene that confers pleiotropic  
A:Reference number: JE0416; MUID:91285426; PMID:2060792  
A:Accession: PEO402  
A:Molecule type: DNA  
A:Residues: 1-258 <HUS>  
A:Cross-references: GB:X53830; NID:94121; PIDN:CAA37826.1; PID:94122  
A>Note: the authors suggested that this protein is unrelated to the pleiotropic drug res  
nown to be a transcriptional activator (see PIR:S16706)  
R:Gentles, S.; Bowman, S.  
submitted to the EMBL Data Library, June 1995  
A:Reference number: S55102  
A:Accession: S55111  
A:Molecule type: DNA  
A:Residues: 1-383 <GEN>  
A:Cross-references: EMBL:Z49810; NID:9854472; PIDN:CAA89944.1; PID:9854482; GSPDB:GN0001  
A:Experimental source: strain AB972  
C:Genetics:  
A:Gene: SGD:ERG6, SED6, MIPS:YML008c  
A:Cross-references: SGD:S0004467; MIPS:YML008c  
A:Map position: 13L  
C:Superfamily: 24-sterol C-methyltransferase; bioc homolog  
C:Keywords: methyltransferase; S-adenosylmethionine  
F:120-224/Domain: bioc homolog <BIOC>

Query Match 57.8%; Score 37; DB 1; Length 383;  
Best Local Similarity 66.7%; Pred. No. 98;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9  
|||: |||  
Db 286 WYDPLTKW 294

RESULT 67  
T39377  
conserved hypothetical protein SPBC12C2.04 - fission yeast (*Schizosaccharomyces pombe*)  
C:Species: *Schizosaccharomyces pombe*  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 28-Jul-2000  
C:Accession: T39377  
R:Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.  
submitted to the EMBL Data Library, September 1995  
A:Reference number: Z21849  
A:Accession: T39377  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-384 <DEV>  
A:Cross-references: EMBL:Z54140; PIDN:CAA90817.1; GSPDB:GN00066; SPDB:SPBC12C2.04  
A:Experimental source: strain 972h-; cosmid c12c2  
C:Genetics:  
A:Gene: SPDB:SPBC12C2.04  
C:Superfamily: *Schizosaccharomyces pombe* hypothetical protein SPAC2B1.17

Query Match 57.8%; Score 37; DB 2; Length 384;  
Best Local Similarity 75.0%; Pred. No. 99;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 8  
|||: |||  
Db 247 WYDPLTKLW 254

RESULT 68  
AH1950  
carbamoyl phosphate synthase small chain [imported] - *Nostoc* sp. (strain PCC 7120)  
C:Species: *Nostoc* sp. PCC 7120  
A>Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120  
C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
C:Accession: AH1950  
R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasanabe, S.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tanaka, S.  
DNA Res. 8, 205-213, 2001  
A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AH1950  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-388 <KAN>  
A:Cross-references: GB:BA000019; PIDN:BA073112.1; PID:91730501; GSPDB:GN00179  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: alr1155  
C:Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain; carbamo

Query Match 57.8%; Score 37; DB 2; Length 388;  
Best Local Similarity 55.6%; Pred. No. 1e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9  
|||: |||  
Db 173 WSDPTTAVW 181

RESULT 69  
BB7503  
acyl-CoA dehydrogenase family protein [imported] - *Caulobacter crescentus*  
C:Species: *Caulobacter crescentus*  
C>Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 03-Aug-2001  
C:Accession: BB7503  
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kjolton, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
 A>Title: Complete Genome Sequence of *Caulobacter crescentus*.  
 A/Reference number: A87249; MUID:21173698; PMID:11259647  
 A/Accession: B87503  
 A>Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-401 <STO>  
 A/Cross-references: GB:AE005673; NID:g13423526; PIDN:AAK24022.1; GSPDB:GN00148  
 C/Genetics:  
 A/Gene: CC2049  
 C/Superfamily: acyl-CoA dehydrogenase

Query Match 57.8%; Score 37; DB 2; Length 401;  
 Best Local Similarity 60.0%; Pred. No. 1e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKML 10  
 ||| |||  
 Db 46 WKRPDAKML 55

RESULT 70  
 H87793  
 protein C27A12.8 [imported] - *Caenorhabditis elegans*  
 C/Species: *Caenorhabditis elegans*  
 C/Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
 C/Accession: H87793  
 R/Anonymous, The C. elegans Sequencing Consortium.  
 Science 282, 2012-2018, 1998  
 A>Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology  
 A/Reference number: A75000; MUID:99069613; PMID:9851916  
 A/Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.elg  
 A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
 A/Accession: H87793  
 A>Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-436 <STO>  
 A/Cross-references: GB:chr\_1; PIDN:AA93645.1; PID:g2105480; GSPDB:GN00019; CESP:C27A12.  
 C/Genetics:  
 A/Gene: C27A12.8  
 A/Map position: 1

Query Match 57.8%; Score 37; DB 2; Length 436;  
 Best Local Similarity 50.0%; Pred. No. 1.1e+02;  
 Matches 7; Conservative 2; Mismatches 1; Indels 4; Gaps 1;

QY 1 WYDP---LTKML 10  
 ||:| |||  
 Db 220 WHEPVNCRILKML 233

RESULT 71  
 A72429  
 oligopeptide ABC transporter, periplasmic oligopeptide-binding protein - *Thermotoga maritima*  
 C/Species: *Thermotoga maritima*  
 C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000  
 C/Accession: A72429  
 R/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.  
 Nature 399, 323-329, 1999  
 A>Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq  
 A/Reference number: A72200; MUID:99287316; PMID:10360571  
 A/Accession: A72429  
 A>Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-606 <ARN>  
 A/Cross-references: GB:AE001690; GB:AE000512; NID:g4980496; PIDN:AAD35125.1; PID:g498051  
 A/Experimental source: strain MSB8  
 C/Genetics:  
 A/Gene: TM0031

C/Superfamily: dipeptide transport protein

Query Match 57.8%; Score 37; DB 2; Length 606;  
 Best Local Similarity 50.0%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKML 10  
 ||:| |||  
 Db 533 WYEXSTKMYI 542

RESULT 72  
 D72306  
 hypothetical protein - *Thermotoga maritima* (strain MSB8)  
 C/Species: *Thermotoga maritima*  
 C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 28-Jul-2000  
 C/Accession: D72306  
 R/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.  
 Nature 399, 323-329, 1999  
 A>Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq  
 A/Reference number: A72200; MUID:99287316; PMID:10360571  
 A/Accession: D72306  
 A>Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-608 <ARN>  
 A/Cross-references: GB:AE001763; GB:AE000512; NID:g4981551; PIDN:AAD36097.1; PID:g4981561  
 A/Experimental source: strain MSB8  
 C/Genetics:  
 A/Gene: TM1020  
 C/Superfamily: *Thermotoga maritima* hypothetical protein TM1020

Query Match 57.8%; Score 37; DB 2; Length 608;  
 Best Local Similarity 60.0%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKML 10  
 ||:| |||  
 Db 201 WYELKLYL 210

RESULT 73  
 H71376  
 probable tpr protein B (tprB) - *Syphilis spirochete*  
 C/Species: *Treponema pallidum* subsp. *pallidum* (*Syphilis spirochete*)  
 C/Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 21-Jan-2000  
 C/Accession: H71376  
 R/Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinn, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; McDor they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
 Science 281, 375-388, 1998  
 A>Title: Complete genome sequence of *Treponema pallidum*, the *Syphilis spirochete*.  
 A/Reference number: A71250; MUID:98332770; PMID:965876  
 A/Accession: H71376  
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-660 <COL>  
 A/Cross-references: GB:AE001186; GB:AE000520; NID:g3322263; PIDN:AA65006.1; PID:g332226  
 A/Experimental source: strain Nichols  
 C/Genetics:  
 A/Gene: TP0011  
 C/Superfamily: *Treponema pallidum* tprL protein

Query Match 57.8%; Score 37; DB 2; Length 660;  
 Best Local Similarity 75.0%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYDPLTKL 8  
 ||| |||  
 Db 485 WYDSLTKL 492

## RESULT 74

JX0338

rabphilin-3A - mouse

N.Alternate names: Rab3A, a ras p21 related small GTP binding protein

C.Species: Mus musculus (house mouse)

C.Date: 22-Apr-1995 #sequence\_revision 26-May-1995 #text\_change 07-May-1999

C.Accession: JX0338

R.Inagaki, N.; Mizuta, M.; Seino, S.

J. Biochem. 116, 239-242, 1994

A.Title: Cloning of a mouse rabphilin-3A expressed in hormone-secreting cells.

A.Reference number: JX0338; PMID:9512445; PMID:782236

A.Accession: JX0338

A.Molecule type: mRNA

A.Residues: 1-681 &lt;INA&gt;

A.Cross-references: DDBJ:D29965

C.Superfamily: protein kinase C C2 region homology

F.373-489/Domain: protein kinase C C2 region homology &lt;KC2A&gt;

F.531-646/Domain: protein kinase C C2 region homology &lt;KC2B&gt;

## Query Match

Best Local Similarity 57.8%; Score 37; DB 2; Length 681;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DPLTKLWL 10

Db 574 DPFVKLWL 581

## RESULT 75

I58166

rabphilin-3A - rat

C.Species: Rattus norvegicus (Norway rat)

C.Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 05-Nov-1999

C.Accession: I58166

R.Li, C.; Takei, K.; Geppert, M.; Daniell, L.; Stenius, K.; Chapman, E.R.; Jahn, R.; De

Neuron 13, 885-898, 1994

A.Title: Synaptic targeting of rabphilin-3A, a synaptic vesicle Ca2+/phospholipid-binding

A.Reference number: I58166; PMID:9503210; PMID:7946335

A.Accession: I58166

A.Status: preliminary; translated from GB/EMBL/DDBJ

A.Molecule type: mRNA

A.Residues: 1-684 &lt;RES&gt;

A.Cross-references: EMBL:U12571; NID:G533710; PIDN:AAA62662.1; PID:G533711

C.Superfamily: protein kinase C C2 region homology

F.376-492/Domain: protein kinase C C2 region homology &lt;KC2A&gt;

F.534-649/Domain: protein kinase C C2 region homology &lt;KC2B&gt;

## Query Match

Best Local Similarity 75.0%; Score 37; DB 2; Length 684;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DPLTKLWL 10

Db 577 DPFVKLWL 584

## RESULT 76

A48097

rabphilin-3A - bovine

C.Species: Bos primigenius taurus (cattle)

C.Date: 21-Jan-1999 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999

C.Accession: A48097

R.Shirataki, H.; Kaibuchi, K.; Sakoda, T.; Kishida, S.; Yamaguchi, T.; Wada, K.; Miyazaki

Mol. Cell. Biol. 13, 2061-2068, 1993

A.Title: Rabphilin-3A, a putative target protein for smg p25A/rab3A p25 small GTP-binding

A.Reference number: A48097; PMID:93204952; PMID:8384302

A.Accession: A48097

A.Status: preliminary; not compared with conceptual translation

A.Molecule type: nucleic acid; protein

A.Residues: 1-704 &lt;SH&gt;

A.Cross-references: GB:D13613; NID:G285645; PIDN:BA002780.1; PID:d1003285; PID:G285646

A.Experimental source: brain

A&gt;Note: sequence extracted from NCBI backbone (NCBIP:127629)

C.Superfamily: protein kinase C C2 region homology

F.396-512/Domain: protein kinase C C2 region homology &lt;KC2A&gt;

F.554-669/Domain: protein kinase C C2 region homology &lt;KC2B&gt;

## Query Match

Best Local Similarity 57.8%; Score 37; DB 2; Length 704;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DPLTKLWL 10

Db 597 DPFVKLWL 604

## RESULT 77

A53714

protein kinase (EC 2.7.1.37) B144 - human

N.Alternate names: GC kinase

C.Species: Homo sapiens (man)

C.Date: 07-Jul-1995 #sequence\_revision 07-Jul-1995 #text\_change 24-Sep-1999

C.Accession: A53714

R.Kacz, P.; Whalen, G.; Kehrl, J.H.

J. Biol. Chem. 269, 16802-16809, 1994

A.Title: Differential expression of a novel protein kinase in human B lymphocytes. Prefe

A.Reference number: A53714; PMID:94266900; PMID:7515885

A.Accession: A53714

A.Status: preliminary

A.Molecule type: mRNA

A.Residues: 1-819 &lt;KAT&gt;

A.Cross-references: GB:U07349; NID:G531819; PIDN:AAA20968.1; PID:G531820

C.Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

C.Keywords: ATP; phosphotransferase

F.13-272/Domain: protein kinase homology &lt;KIN&gt;

F.21-29/Region: protein kinase ATP-binding motif

## Query Match

Best Local Similarity 57.8%; Score 37; DB 2; Length 819;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10

Db 626 WYEPLOKFL 635

## RESULT 78

T37789

Scd1 protein - fission yeast (Schizosaccharomyces pombe)

C.Species: Schizosaccharomyces pombe

C.Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Nov-2000

C.Accession: T37789

R.Oliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

Submitted to the EMBL Data Library, September 1995

A.Reference number: Z21746

A.Accession: T37789

A.Status: preliminary; translated from GB/EMBL/DDBJ

A.Molecule type: DNA

A.Residues: 1-872 &lt;OUT&gt;

A.Cross-references: EMBL:Z99529; PIDN:CAB11037.1; GSPDB:GN00066; SPDB:SPAC16E8.09

A.Experimental source: strain 972h(-); cosmid c16E8

R.Chang, E.C.; Barr, M.; Wang, Y.; Jung, V.; Xu, H.P.; Wigler, M.H.

Cell 79, 131-141, 1994

A.Title: Cooperative interaction of S. pombe proteins required for mating and morphogene

A.Reference number: Z09915

A.Accession: T52450

A.Status: preliminary; translated from GB/EMBL/DDBJ

A.Molecule type: DNA

A.Residues: 1-872 &lt;CHA&gt;

A.Cross-references: EMBL:U12538; PIDN:AAA50556.2

C.Genetics: SPDB:SPAC16E8.09; scd1

A.Map position: 9/1

C.Function:

A&gt;Description: required for normal morphology and mating

Query Match 57.8%; Score 37; DB 2; Length 872;  
Best Local Similarity 62.5%; Pred. No. 2.3e+02;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DPLTKLWL 10  
||:|:|  
Db 105 DPVTEIWL 112

## RESULT 79

hypothetical protein DKFp434N074.1 - human (fragments)  
C/Species: Homo sapiens (man)  
C/Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 03-Nov-2000  
C/Accession: T12545  
R/Wandut, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, June 1999  
A/Reference number: Z17524  
A/Accession: T12545  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-677,678-965 <NAN>  
A/Cross-references: EMBL:AL096732  
A/Experimental source: adult testis; clone DKFp434N074  
A/Note: the cDNA sequence contains a -1 frameshift near codon 677  
C/Genetics:  
A/Note: DKFp434N074.1  
C/Superfamily: dynein heavy chain, ciliary

Query Match 57.8%; Score 37; DB 2; Length 965;  
Best Local Similarity 66.7%; Pred. No. 2.6e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKLWL 10  
|||:|:|  
Db 892 YDPLPIWL 900

## RESULT 80

DJBE11  
DNA-directed DNA polymerase (EC 2.7.7.7) - ictalurid herpesvirus 1 (strain auburn 1)  
C/Species: ictalurid herpesvirus 1  
A/Note: host ictalurid punctatus (channel catfish)  
C/Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 11-Jun-1999  
C/Accession: D36792  
R/Davison, A.J.  
submitted to GenBank, January 1992  
A/Description: Channel catfish virus: a new type of herpesvirus.  
A/Reference number: A36804  
A/Accession: D36792  
A/Molecule type: DNA  
A/Residues: 1-985 <NAV>  
A/Cross-references: GB:M75136; NID:G331209; PIDN:AAA88160.1; PID:G331267  
R/Davison, A.J.  
Virology 186, 9-14, 1992  
A/Title: Channel catfish virus: a new type of herpesvirus.  
A/Reference number: A39447; MUID:92087490; PMID:11727613  
A/Contents: annotation  
A/Note: neither amino acid nor nucleotide sequence is given  
C/Genetics:  
A/Genes: 57  
C/Superfamily: ictalurid herpesvirus DNA-directed DNA polymerase  
C/Keywords: DNA replication; nucleotidyltransferase

Query Match 57.8%; Score 37; DB 1; Length 985;  
Best Local Similarity 50.0%; Pred. No. 2.7e+02;  
Matches 6; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

Qy 1 WY--DPLTKLWL 10  
|:|:|:|  
Db 893 WVVVDPLTGIMM 904

RESULT 81  
YegE protein - Escherichia coli (strain K-12)  
C/Species: Escherichia coli  
C/Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 17-Mar-2003  
C/Accession: B64973  
R/Blatner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Coi

A.; Rose, D.J.; Mau, B.; Sphao, Y.  
Science 277, 1453-1462, 1997  
A/Title: The complete genome sequence of Escherichia coli K-12.  
A/Reference number: A64720; MUID:97426617; PMID:9278503  
A/Accession: B64973  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA

A/Residues: 1-1105 <BLAT>  
A/Cross-references: GB:AE00296; GB:U00096; NID:G1788373; PIDN:AACT5128.1; PID:G1788381;  
A/Experimental source: strain K-12, substrain MG1655  
C/Genetics:  
A/Genes: YegE  
C/Superfamily: signal transduction protein with an integral membrane domain and Pas, GGDI

Query Match 57.8%; Score 37; DB 2; Length 1105;  
Best Local Similarity 58.3%; Pred. No. 3e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 WYDPLTKL--WL 10  
||:|:| |  
Db 114 WYDPLQNLADWL 125

## RESULT 82

T30291  
dextranase - Streptococcus sobrinus  
C/Species: Streptococcus sobrinus  
C/Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 22-Oct-1999  
C/Accession: T30291  
R/Wanda, S.Y.; Curtiss III, R.  
J. Bacteriol. 176, 3839-3850, 1994  
A/Title: Purification and characterization of Streptococcus sobrinus dextranase produced  
A/Reference number: Z20810; MUID:94292401; PMID:8021165  
A/Accession: T30291  
A/Status: preliminary; translated from GB/EMBL/DDBJ  
A/Molecule type: DNA  
A/Residues: 1-1337 <NAN>  
A/Cross-references: EMBL:M06978; NID:G450640; PID:G450641; PIDN:AAA21772.1

Query Match 57.8%; Score 37; DB 2; Length 1337;  
Best Local Similarity 55.6%; Pred. No. 3.7e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WYDPLTKLW 9  
|:|:|:|  
Db 423 YNPTSKLW 431

## RESULT 83

C75250  
hypothetical protein - Deinococcus radiodurans (strain R1)  
C/Species: Deinococcus radiodurans  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 26-May-2000  
C/Accession: C75250  
R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A/Title: Genome sequence of the radioreistant bacterium Deinococcus radiodurans R1.  
A/Reference number: A75250; MUID:20036896; PMID:10567266  
A/Accession: C75250  
A/Status: preliminary  
A/Molecule type: DNA

A/Residues: 1-222 <WHI>  
A/Cross-references: GB:AE002092; GB:AE000513; NID:G6460455; PIDN:AAF12174.1; PID:G646046

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR2628

A:Map position: 1

C:Superfamily: Deinococcus radiodurans hypothetical protein DR2628

Query Match 57.0%; Score 36.5; DB 2; Length 222;

Best Local Similarity 72.7%; Pred. No. 68; Indels 1; Gaps 1;

Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 WYDPLTKLWL 10  
| | | | |  
| | | | |  
DB 9 WSAPLTKLWL 19

RESULT 84

E87706

prolyl oligopeptidase family protein [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001

C:Accession: E87706

R:Nielsen, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

n, J.; Esmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: E87706

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-723 <STO>

A:Crosss-references: GB:AB005673; NID:G13425449; PIDN:AAK25649.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC3687

Query Match 57.0%; Score 36.5; DB 2; Length 723;

Best Local Similarity 80.0%; Pred. No. 2,3e+02; Indels 1; Gaps 1;

Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 YDPLTKLWL 10  
| | | | |  
| | | | |  
DB 511 YDPLTKLWL 520

RESULT 85

S72842

methionine synthase meth2 - Mycobacterium leprae

N:Alternate names: B2126 Cl 157 protein

C:Species: Mycobacterium leprae

C:Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 23-Mar-2001

C:Accession: S72842

R:Smith, D.R.; Robinson, K.

submitted to the EMBL Data Library, November 1993

A:Description: Mycobacterium leprae cosmid B2126.

A:Reference number: S72585

A:Accession: S72842

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-867 <SMI>

A:Crosss-references: EMBL:U00017; NID:G466994; PIDN:AAA17182.1; PID:G466997

C:Genetics:

A:Gene: meth2

A:Start codon: GTG

Query Match 57.0%; Score 36.5; DB 2; Length 867;

Best Local Similarity 80.0%; Pred. No. 2,8e+02; Indels 1; Gaps 1;

Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 YDPLTKLWL 10  
| | | | |  
| | | | |  
DB 598 YDPLTKLWL 607

RESULT 86

E87072

hypothetical protein meth [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001

C:Accession: E87072

R:Coile, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho-

em, M.A.; Rutherford, K.M.

R.; Davies, R.M.; Devlin, K.; Duthey, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

Nature 409, 1007-1011, 2001

A:Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A86909; MUID:21128732; PMID:11234002

A:Accession: E87072

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1206 <STO>

A:Crosss-references: GB:AL450380; NID:G13093228; PIDN:CAC31688.1; GSPDB:GN00147

C:Genetics:

A:Gene: meth

C:Superfamily: cobalamin-dependent methionine synthase; cobalamin-binding homology

Query Match 57.0%; Score 36.5; DB 2; Length 1206;

Best Local Similarity 80.0%; Pred. No. 4e+02; Indels 1; Gaps 1;

Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 YDPLTKLWL 10  
| | | | |  
| | | | |  
DB 620 YDPLTKLWL 629

RESULT 87

AG1129

hypothetical protein lmo0438 [imported] - Listeria monocytogenes (strain EGD-e)

C:Species: Listeria monocytogenes

C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001

C:Accession: AG1129

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bioecker

; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fsihi, H.

D.; Jones, L.M.; Karel, U.

Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkay, G.; Madueno, E.; Maitournam, A.; Ma-

ok, C.; Schueter, T.; Simoes, N.; Tietzer, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A:Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AG1129

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-205 <GLA>

A:Crosss-references: GB:NC\_003210; PIDN:CAC98517.1; PID:G16409815; GSPDB:GN00177

A:Experimental source: strain EGD-e

C:Genetics:

A:Gene: lmo0438

Query Match 56.2%; Score 36; DB 2; Length 205;

Best Local Similarity 44.4%; Pred. No. 76; Indels 0; Gaps 0;

Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 9  
| | | | |  
| | | | |  
DB 7 WFNGLSKMW 15

RESULT 88

I76659

pregnancy-specific glycoprotein - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 23-Jul-1999

C:Accession: I76659

R:Rudert, F.; Saunders, A.M.; Thompson, J.A.; Rebstock, S.; Zimmermann, W.A.

Mamm. Genome 3, 262-273, 1992

A:Title: Characterization of murine carcinoembryonic antigen gene family members.

A:Reference number: I57007; MUID:92345715; PMID:1638085

A:Accession: I76669  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-209 <RES>  
 A:Cross-references: GB:M83346; NID:g200318; PIDN:AAA39917.1; PID:g200319  
 C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi  
 C:Keywords: glycoprotein  
 F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA1>

Query Match 56.2%; Score 36; DB 2; Length 209;  
 Best Local Similarity 55.6%; Pred. No. 77;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9  
 |||  
 67 WYRGMTNLW 75

RESULT 89  
 T50960  
 related to modulation protein nobB [imported] - Neurospora crassa  
 N:Alternate names: protein B24P7.150  
 C:Species: Neurospora crassa  
 C>Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 21-Jul-2000  
 C:Accession: T50960  
 R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Partmann, B.; Holland, R.; Nyakatura,  
 submitted to the Protein Sequence Database, July 2000  
 A:Reference number: Z52586  
 A:Accession: T50960  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-312 <SCH>  
 A:Cross-references: EMBL:AL389890; GSPDB:GN00116; NCSP:B24P7.150  
 A:Experimental source: BAC clone B24P7; strain OR74A  
 C:Genetics:  
 A:Gene: NCSP:B24P7.150  
 A:Map position: 6

Query Match 56.2%; Score 36; DB 2; Length 312;  
 Best Local Similarity 60.0%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 10  
 |||  
 64 WTDVLMRLW 73

RESULT 90  
 D64233  
 hypothetical protein MG302 - Mycoplasma genitalium  
 C:Species: Mycoplasma genitalium  
 C>Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 07-Dec-1999  
 C:Accession: D64233  
 R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;  
 M.; Fuhrman, J.; Nguyen, D.; Uettermann, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.  
 C.A.; Venter, J.C.  
 Science 270: 397-403, 1995  
 A>Title: The minimal gene complement of Mycoplasma genitalium.  
 A:Reference number: A64200; MUID:96026346; PMID:7569993  
 A:Accession: D64233  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-317 <TIGR>  
 A:Cross-references: GB:U9711; GB:I43967; NID:g1045997; PID:g1046001; TIGR:MG302  
 A:Experimental source: strain G-37  
 C:Genetics:  
 A:Genetic code: SGC3

Query Match 56.2%; Score 36; DB 2; Length 317;  
 Best Local Similarity 85.7%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 DPLTKLW 9

DB 11 DPLTKLW 17  
 |||  
 |||

RESULT 91  
 S59388  
 Probable membrane protein YLR242c - yeast (Saccharomyces cerevisiae)  
 N:Alternate names: hypothetical protein L9672.11  
 C:Species: Saccharomyces cerevisiae  
 C>Date: 30-Nov-1995 #sequence\_revision 23-Feb-1996 #text\_change 06-Feb-1998  
 C:Accession: S59388  
 R:Johnson, D.  
 submitted to the EMBL Data Library, February 1995  
 A:Description: The sequence of S. cerevisiae cosmid 9672.  
 A:Reference number: S59386  
 A:Accession: S59388  
 A:Molecule type: DNA  
 A:Residues: 1-321 <JOH>  
 A:Cross-references: EMBL:U20865; NID:g662330; PID:g662341; MIPS:YLR242C  
 A:Experimental source: strain S288C (AB972)  
 C:Genetics:  
 A:Gene: SGD:ARY1  
 A:Cross-references: SGD:S0004232; MIPS:YLR242C  
 A:Map position: 12R  
 C:Keywords: transmembrane protein  
 F:40-56/Domain: transmembrane #status predicted <TM1>  
 F:218-234/Domain: transmembrane #status predicted <TM2>  
 F:276-292/Domain: transmembrane #status predicted <TM3>

Query Match 56.2%; Score 36; DB 2; Length 321;  
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLW 10  
 |||  
 102 YDRLNRLW 110

RESULT 92  
 H82632  
 Arpase XF1828 [imported] - Xylella fastidiosa (strain 9a5c)  
 C:Species: Xylella fastidiosa  
 C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Sep-2000  
 C:Accession: H82632  
 R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc  
 Nature 406: 151-157, 2000  
 A>Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
 A:Reference number: A82515; MUID:20365717; PMID:10910347  
 A>Note: for a complete list of authors see reference number A59328 below  
 A:Accession: H82632  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-405 <SIM>  
 A:Cross-references: GB:AE004004; GB:AE003849; NID:g9106905; PIDN:AAF84634.1; GSPDB:GN001;  
 A:Experimental source: strain 9a5c  
 R:Simpson, A.J.C.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al  
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carter, H  
 as-Nero, E.; Docena, C.; El-Porri, H.; Facincani, A.P.; Ferreira, A.J.S.  
 submitted to GenBank, June 2000  
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm  
 J.D.; D'Unquella, M.L.; Kemper, E.L.; Kitajima, J.P.; Klieger, J.E.; Kuramae, E.E.; Laigri  
 chado, M.A.; Martins, E.M.F.; Matukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;  
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.  
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki  
 A.; Antunes da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira  
 M.; Teunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
 A:Reference number: A59328  
 A:Contents: annotation  
 C:Genetics:  
 A:Gene: XF1828  
 C:Superfamily: Neisseria meningitidis probable nucleotide-binding protein NMA1520

Query Match 56.2%; Score 36; DB 2; Length 405;  
Best Local Similarity 55.6%; Pred. No. 1.6e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9  
|:|:|:|:|  
Db 62 WMDRFTALM 70

## RESULT 93

T47818  
hypothetical protein P24G16.210 - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C/Accession: T47818  
R/D Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.;  
submitted to the Protein Sequence Database, February 2000  
A/Reference number: Z24477  
A/Accession: T47818  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-418 <DAN>  
A/Cross-references: EMBL:AL138647  
A/Experimental source: cultivar Columbia; BAC clone P24G16  
C/Genetics:  
A/Map position: 3  
A/Note: P24G16.210

Query Match 56.2%; Score 36; DB 2; Length 418;  
Best Local Similarity 62.5%; Pred. No. 1.6e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9  
|:|:|:|:|  
Db 280 YDPTNSW 287

## RESULT 94

SS1715  
hypothetical protein - Chlamydia trachomatis (fragment)  
C/Species: Chlamydia trachomatis  
C/Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 11-Jan-2000  
C/Accession: SS1715  
R/Pohlner, J.  
submitted to the EMBL Data Library, April 1994  
A/Description: Sequence of the recA gene from Chlamydia trachomatis L2.  
A/Reference number: SS1714  
A/Accession: SS1715  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-419 <POH>  
A/Cross-references: EMBL:Z3530; NID:G607060; PIDN:CAA83540.1; PID:G607062  
C/Superfamily: Chlamydia hypothetical protein CT648

Query Match 56.2%; Score 36; DB 2; Length 419;  
Best Local Similarity 85.7%; Pred. No. 1.6e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTK 7  
|:|:|:|:|  
Db 236 YDPLTK 242

## RESULT 95

F71488  
hypothetical protein CT648 - Chlamydia trachomatis (serotype D, strain UW3/Cx)  
C/Species: Chlamydia trachomatis  
C/Date: 13-Sep-1998 #sequence\_revision 13-Sep-1998 #text\_change 10-Dec-1999  
C/Accession: F71488  
R/Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998  
A/Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis  
A/Reference number: A1570; MUID:9900809; PMID:9784136

A/Accession: F71488  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-424 <ARN>  
A/Cross-references: GB:AE001335; GB:AE001273; NID:G3329091; PIDN:AA68825.1; PID:G332909  
A/Experimental source: serotype D, strain UW-3/Cx  
C/Genetics:  
A/Gene: CT648  
C/Superfamily: Chlamydia hypothetical protein CT648

Query Match 56.2%; Score 36; DB 2; Length 424;  
Best Local Similarity 85.7%; Pred. No. 1.6e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTK 7  
|:|:|:|:|  
Db 241 YDPLTK 247

## RESULT 96

A64945  
probable membrane protein b1833 - Escherichia coli (strain K-12)  
C/Species: Escherichia coli  
C/Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
C/Accession: A64945  
R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col  
A.; Rose, D.V.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A/Title: The complete genome sequence of Escherichia coli K-12.  
A/Reference number: A64720; MUID:9742617; PMID:9278503  
A/Accession: A64945  
A/Status: nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-427 <BLAT>  
A/Cross-references: GB:AE000277; GB:U00096; NID:G1788129; PIDN:AACT4903.1; PID:G1788137;  
A/Experimental source: strain K-12, substrain MG1655  
C/Superfamily: hypothetical protein H1671  
C/Keywords: transmembrane protein  
F/69-85/Domain: transmembrane #status predicted <TM1>  
F/120-136/Domain: transmembrane #status predicted <TM2>  
F/163-179/Domain: transmembrane #status predicted <TM3>  
F/189-205/Domain: transmembrane #status predicted <TM4>  
F/274-290/Domain: transmembrane #status predicted <TM5>  
F/311-327/Domain: transmembrane #status predicted <TM6>  
F/390-406/Domain: transmembrane #status predicted <TM7>

Query Match 56.2%; Score 36; DB 2; Length 427;  
Best Local Similarity 50.0%; Pred. No. 1.6e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKML 10  
|:|:|:|:|  
Db 84 WGEPLHIWL 93

## RESULT 97

C85795  
hypothetical protein Z2880 [imported] - Escherichia coli (strain O157:H7, substrain EDL93;  
C/Species: Escherichia coli  
C/Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C/Accession: C85795  
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,  
Hiller, L.; Grobeck, E.D.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A/Reference number: A85480; MUID:21074935; PMID:11206551  
A/Accession: C85795  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-427 <STO>  
A/Cross-references: GB:AE005174; NID:G12515883; PIDN:AA656823.1; GSPDB:GN00145; UMGF:Z2880  
A/Experimental source: strain O157:H7, substrain EDL933  
C/Genetics:

A:Gene: Z2880  
A:Superfamily: hypothetical protein H11671  
Query Match 56.2%; Score 36; DB 2; Length 427;  
Best Local Similarity 50.0%; Pred. No. 1.6e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
OY 1 WYDPLTKLWL 10  
DB 84 WGEPLHLIWL 93  
RESULT 98  
G90946  
probable membrane protein EC62543 [similarity] - Escherichia coli (strain O157:H7, subst  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 02-Nov-2001  
C:Accession: G90946  
C:Authors: T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
G.; Hayashi, T.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
A:Reference number: A99629; PMID:21156231; PMID:11258796  
A:Accession: G90946  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-427 <HAY>  
A:Cross-references: GB:BA000007; PIDN:BA835966.1; PID:G13362010; GSPDB:GN00154  
A:Experimental source: strain O157:H7, substrain RIMD 0509952  
A:Genetics: A:Gene: EC62543  
C:Superfamily: hypothetical protein H11671  
Query Match 56.2%; Score 36; DB 2; Length 427;  
Best Local Similarity 50.0%; Pred. No. 1.6e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
OY 1 WYDPLTKLWL 10  
DB 84 WGEPLHLIWL 93  
RESULT 99  
JQ1864  
hypothetical 47.0K protein - bovine adenovirus 3  
C:Species: Mastadenovirus bovis (bovine adenovirus 3)  
C:Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 07-May-1999  
C:Accession: JQ1864  
R:Mitral, S.K.; Prevec, L.; Babink, L.A.; Graham, F.L.  
J. Gen. Virol. 73, 3295-3300, 1992  
A:Title: Sequence analysis of bovine adenovirus type 3 early region 3 and fibre protein  
A:Reference number: PQ0499; PMID:93107871; PMID:1469367  
A:Accession: JQ1864  
A:Molecule type: DNA  
A:Residues: 1-428 <MIT>  
A:Cross-references: DDBJ:DJ2928  
A:Experimental source: strain WBR-1  
A:Note: the authors described cardiolipin binding site for residue 67  
Query Match 56.2%; Score 36; DB 2; Length 428;  
Best Local Similarity 66.7%; Pred. No. 1.6e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
OY 2 YDPLTKLWL 10  
DB 66 YNPPTVLMWL 74  
RESULT 100  
G82847  
hypothetical protein XF0106 [imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 14-Jul-2003

C:Accession: G82847  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; PMID:20365717; PMID:10910347  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: G82847  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-460 <SIM>  
A:Cross-references: GB:AE003864; GB:AE003849; NID:99104879; PIDN:AAFE2919.1; GSPDB:GN001;  
A:Experimental source: strain 9a5c  
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A  
B:Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to Genbank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuratae, E.E.; Laigre  
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, E  
A:Authors: Martins, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeiri, D.A  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, V.E.; de Sa, R.G.; Santelli, R.V.; Sawaaki  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics: A:Gene: XF0106  
C:Superfamily: alpha-L-fucosidase  
Query Match 56.2%; Score 36; DB 2; Length 460;  
Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
OY 2 YDPLTKLWL 10  
DB 180 YGPLTEWML 188

Search completed: July 12, 2004, 21:30:55  
Job time : 27 secs







ID	POL_JSRV	STANDARD	PRT	870 AA.
253	32	50.0	492	1
254	32	50.0	492	1
255	32	50.0	492	1
256	32	50.0	492	1
257	32	50.0	492	1
258	32	50.0	492	1
259	32	50.0	492	1
260	32	50.0	492	1
261	32	50.0	492	1
262	32	50.0	492	1
263	32	50.0	492	1
264	32	50.0	492	1
265	32	50.0	492	1
266	32	50.0	492	1
267	32	50.0	492	1
268	32	50.0	492	1
269	32	50.0	492	1
270	32	50.0	492	1
271	32	50.0	492	1
272	32	50.0	492	1
273	32	50.0	492	1
274	32	50.0	492	1
275	32	50.0	492	1
276	32	50.0	492	1
277	32	50.0	492	1
278	32	50.0	492	1
279	32	50.0	492	1
280	32	50.0	492	1
281	32	50.0	492	1
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292	32	50.0	492	1
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294	32	50.0	492	1
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297	32	50.0	492	1
298	32	50.0	492	1
299	32	50.0	492	1
300	32	50.0	492	1

## ALIGNMENTS

RESULT 1  
POL\_JSRV STANDARD; PRT: 870 AA.  
AC P31623;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DE POL polypeptide (Contains: Reverse transcriptase (EC 2.7.7.49);  
Endonuclease).  
GN Sheep pulmonary adenomatosis virus (Jaagsiekte sheep retrovirus)  
OS (JRSV).  
OC Viruses; Retrovirdae; Retroviridae; Betaretrovirus.  
OX NCB1\_Taxid=11746;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92333675; PubMed=1629959;  
RA York D.F., Vigne R., Verwoerd D.W., Querat G.;  
RT "Nucleotide sequence of the jaagsiekte retrovirus, an exogenous and  
endogenous type D and B retrovirus of sheep and goats.";

RL J. Virol. 66:4930-4939(1992).  
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate  
CC + {DNA}(N).  
CC -1- PFM: Specific enzymatic cleavages in vivo yield mature proteins.  
CC -1- MISCELLANEOUS: THIS PROTEIN IS PROBABLY EXPRESSED AS A FUSED  
GAG-POL-POL POLYPEPTIDE BY A RIBOSOMAL FRAMESHIFTING.  
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CC -----  
CC EMBL: M80216; AAA89182.1; ALT\_INIT.  
CC PIR: C42740; GNMVJA.  
CC HSSP: P03355; 1MML.  
CC InterPro: IPR001037; Integrase\_C.  
CC InterPro: IPR003308; Integrase\_Zn.  
CC InterPro: IPR002156; RNaseH.  
CC InterPro: IPR001584; Rve.  
CC InterPro: IPR000477; RYase.  
CC Pfam: PF00552; Integrase; 1.  
CC Pfam: PF02022; Integrase\_Zn; 1.  
CC Pfam: PF00075; RNaseH; 1.  
CC Pfam: PF00665; rve; 1.  
CC Pfam: PF00078; rve; 1.  
CC Transferrase; RNA-directed DNA polymerase; Hydrolase; Nuclease;  
KW Endonuclease; Polypeptide.  
SQ SEQUENCE 870 AA; 99312 MW; CFADEAFB879C033 CRC64;

Query Match 71.9%; Score 46; DB 1; Length 870;  
Best local similarity 77.8%; Pred. No. 4.3;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
DB 1 WYDPTKLM 9  
813 WKDPTNLM 821

RESULT 2  
YEDO\_SALTI STANDARD; PRT: 567 AA.  
AC Q825R0;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DE Hypothetical protein yedQ.  
GN YEDO OR STY2194 OR T0891.  
OS Salmonella typhi.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Salmonella.  
OX NCB1\_Taxid=601;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CT18;  
RX MEDLINE=21534947; PubMed=11677608;  
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,  
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,  
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,  
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
RA Fellwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jaseis K.,  
RA Krogh A., Larsen T.S., Leach S., Mout R., O'Gaora P., Parry C.,  
RA Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
RA Whitehead S., Barrrell B.G.;  
RT "Complete genome sequence of a multiple drug resistant Salmonella  
enterica serovar Typhi CT18.";  
RL Nature 413:848-852(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Ty2 / ATCC 700931;  
RX MEDLINE=22531367; PubMed=12644504;

```
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Butland V., Kodoyianni V., Schwartz D.C., Blatner F.R.,
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18."
RL J. Bacteriol. 185:2330-2337(2003).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE YALC / YFIN (E.COLI), YHCK (B.SUBTILIS)
CC FAMILY.
CC -1- SIMILARITY: Contains 1 GDBF domain.
CC -----
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CC -----
DR EMBL; AL672727; CAD05734.1; -
DR EMBL; AE016837; AA068569.1; -
DR InterPro; IPR00160; GDBF.
DR Pfam; PF00990; GDBF; 1.
DR SMART; SM00267; DUF1; 1.
DR TIGRfams; TIGR00254; GDBF; 1.
DR PROSITE; PS50887; GDBF; 1.
DR Hypothetical protein; Transmembrane; Complete proteome.
KM TRANSMEM 20 40 POTENTIAL.
FT TRANSMEM 357 377
FT DOMAIN 425 560 GDBF.
SQ SEQUENCE 567 AA; 65099 MW; 9E1AE3768ADAD6D CRC64;

Query Match 67.2%; Score 43; DB 1; Length 567;
Best Local Similarity 66.7%; Pred. No. 8.8;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLM 9
Db 396 WHDPLTKLY 404

RESULT 3
YEDQ_SALTY STANDARD; PRT; 570 AA.
ID YEDQ_SALTY STANDARD; PRT; 570 AA.
AC 08ZNT5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein yedQ.
GN YEDQ OR STM1987.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN NCBI_TaxID=602;
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvanev E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RA "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2."
RL Nature 413:852-856(2001).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE YALC / YFIN (E.COLI), YHCK (B.SUBTILIS)
CC FAMILY.
CC -1- SIMILARITY: Contains 1 GDBF domain.
CC -----
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CC -----
DR EMBL; AE008788; AA120897.1; -
DR StyGene; SG72727; yedQ.
DR InterPro; IPR00160; GDBF.
DR Pfam; PF00990; GDBF; 1.
DR SMART; SM00267; DUF1; 1.
DR TIGRfams; TIGR00254; GDBF; 1.
DR PROSITE; PS50887; GDBF; 1.
KM Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 20 40 POTENTIAL.
FT TRANSMEM 360 380
FT DOMAIN 428 563 GDBF.
SQ SEQUENCE 570 AA; 65429 MW; BF8FDF0CF894925 CRC64;

Query Match 67.2%; Score 43; DB 1; Length 570;
Best Local Similarity 66.7%; Pred. No. 8.9;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLM 9
Db 399 WHDPLTKLY 407

RESULT 4
POL_SMRVH STANDARD; PRT; 888 AA.
ID POL_SMRVH STANDARD; PRT; 888 AA.
AC P03364;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE POL polypeptide [Contains: Reverse transcriptase (EC 2.7.7.49);
DE Endonuclease].
GN POL.
OS Squirrel monkey retrovirus (SMRV-H) (SMRV-HLB).
OC Viruses; Retrovirus; Retroviridae; Betaretrovirus.
OX NCBI_TaxID=11856;
RN NCBI_TaxID=11856;
RP SEQUENCE FROM N.A.
RC MEDLINE=89073750; PubMed=3201749;
RA Oda T., Ikeda S., Watanabe S., Hatsuoka M., Akiyama K.,
RA Mitsuoka F.;
RT "Molecular cloning, complete nucleotide sequence, and gene structure
RT of the provirus genome of a retrovirus produced in a human
RT lymphoblastoid cell line."
RL Virology 167:468-476(1988).
RN [2]
RP SEQUENCE OF 595-774 FROM N.A.
RX MEDLINE=84097535; PubMed=6197754;
RA Chiu I.-W., Callahan R., Tronick S.R., Schlom J., Aaronson S.A.;
RA "Major pol gene progenitors in the evolution of oncoviruses."
RL Science 223:364-370(1984).
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {DNA} (N).
CC -----
CC -1- PRT: Specific enzymatic cleavages in vivo yield mature proteins.
CC -----
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CC -----
DR EMBL; K01706; AAA46815.1; -
DR EMBL; M23385; AAA66453.1; ALT_INIT.
DR PIR; A05072; A05072.
DR PIR; C31827; GNLJHD.
DR HSSP; P03355; INML.
DR InterPro; IPR001037; Integrase_C.
```

DR InterPro: IPR003108; Integrase\_Zn.  
 DR InterPro: IPR002156; RNaseH.  
 DR InterPro: IPR001584; Rve.  
 DR InterPro: IPR000477; RVTse.  
 DR Pfam: PF00552; Integrase\_1.  
 DR Pfam: PF02022; Integrase\_Zn; 1.  
 DR Pfam: PF00075; rnsel; 1.  
 DR Pfam: PF00078; rvt; 1.  
 DR Transferrase; RNA-directed DNA polymerase; Hydrolyase; Nuclease;  
 KM Endonuclease; Polypotein.  
 SQ SEQUENCE 888 AA; 99165 MW; B6B2CD09C651B98B CRC64;

Query Match  
 Best Local Similarity 67.2%; Score 43; DB 1; Length 888;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 WYDPLTKLM 9  
 DB 821 WRDPLTSW 829

RESULT 5  
 ID IPP\_HUMAN STANDARD; PRT; 584 AA.  
 AC 09Y573;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Actin-binding protein IPP (MIPP protein).  
 GN IPP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=99173871; PubMed=10072760;  
 RA Kim I.F., Mohammad E., Huang R.C.;  
 RT "Isolation and characterization of IPP, a novel human gene encoding an  
 actin-binding, kelch-like protein.";  
 RL Gene 228:73-83(1999).

CC -!- FUNCTION: May play a role in organizing the actin cytoskeleton.  
 CC -!- SIMILARITY: Contains 1 BTB/POZ domain.  
 CC -!- SIMILARITY: Contains 6 Kelch repeats.

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CC -----  
 DR EMBL: AF156857; AAD39007.1; -.  
 DR Genew; HGNC:6108; IPP.  
 DR MIM; 147485; -.  
 DR GO; GO:0015629; C:actin cytoskeleton; TAS.  
 DR GO; GO:0003779; F:actin binding; TAS.  
 DR InterPro: IPR000210; BTB\_POZ.  
 DR InterPro: IPR006651; Kelch.  
 DR InterPro: IPR006652; Kelch\_rep.  
 DR Pfam; PF00651; BTB; 1.  
 DR Pfam; PF01344; Kelch; 6.  
 DR PRINTS; PR00501; KELCHREPEAT.  
 DR SMART; SMO0225; BTB; 1.  
 DR SMART; SMO0612; Kelch; 6.  
 DR PROSITE; PS50097; BTB; 1.  
 KM Cytoskeleton; Actin-binding; Kelch repeat; Repeat.  
 FT DOMAIN 37 104 BTB.  
 FT REPEAT 289 343 KELCH 1.  
 FT REPEAT 344 390 KELCH 2.

FT REPEAT 391 437 KELCH 3.  
 FT REPEAT 439 485 KELCH 4.  
 FT REPEAT 487 533 KELCH 5.  
 FT REPEAT 535 583 KELCH 6.  
 SQ SEQUENCE 584 AA; 65260 MW; C63EF25D74924AB8 CRC64;

Query Match  
 Best Local Similarity 75.0%; Score 40; DB 1; Length 584;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 YDPLTKLM 9  
 DB 363 YDPVTKQM 370

RESULT 6  
 ID IPP\_MOUSE STANDARD; PRT; 584 AA.  
 AC P28575;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Actin-binding protein IPP (MIPP protein) (Murine IAP-promoted  
 placenta-expressed protein).  
 GN IPP OR MIPP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=21427516; PubMed=11536049;  
 RA Vanhouten J.N., Asch H.L., Asch B.B.;  
 RT "Cloning and characterization of ectopically expressed transcripts  
 for the actin-binding protein MIPP in mouse mammary carcinomas.";  
 RL Oncogene 20:5366-5372(2001).

CC -!- FUNCTION: May play a role in organizing the actin cytoskeleton.  
 CC -!- SIMILARITY: Contains 1 BTB/POZ domain.  
 CC -!- SIMILARITY: Contains 6 Kelch repeats.

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CC -----  
 DR EMBL: AF285178; AAK00278.1; -.  
 DR EMBL; X58523; CAA41413.1; -.  
 DR EMBL; X58524; CAA41414.1; ALT\_SEQ.  
 DR PIR; S16442; S16442.  
 DR MGD; MGI:96581; IPP.  
 DR InterPro: IPR000210; BTB\_POZ.  
 DR InterPro: IPR006652; Kelch\_rep.  
 DR Pfam; PF00651; BTB; 1.  
 DR Pfam; PF01344; Kelch; 6.  
 DR SMART; SMO0225; BTB; 1.  
 DR SMART; SMO0612; Kelch; 6.  
 DR PROSITE; PS50097; BTB; 1.  
 KM Cytoskeleton; Actin-binding; Kelch repeat; Repeat.  
 FT DOMAIN 37 104 BTB.  
 FT REPEAT 296 343 KELCH 1.  
 FT REPEAT 344 390 KELCH 2.  
 FT REPEAT 391 437 KELCH 3.



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CC -----  
DR EMBL, D10483: BAB96514.1; -  
DR EMBL, AE000115: AAC73157.1; -  
DR EMBL, AE016755: AAN78552.1; -  
DR PIR, P64725: P64725.  
DR HSSP, P16083: IOR2.  
DR Ecogen, BG11568: keff.  
DR HAMAP, MF\_01414: -; 1.  
DR InterPro, IPR003680: NADHdh\_2.  
DR Pfam, PF02525: Flavodoxin\_2; 1.  
DR Complete proteome.  
KM CONFLICT 79 79 D -> N (IN REF. 1).  
FT CONFLICT 123 123 V -> G (IN REF. 1).  
SQ SEQUENCE 176 AA; 20170 MW; F641B3952F4EFC41 CRC64;  
  
Query Match 60.9%; Score 39; DB 1; Length 176;  
Best Local Similarity 58.3%; Pred. No. 13;  
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;  
  
QY 1 WYD--PLTKLWL 10  
DB 67 WYSVPLTKLWL 78  
  
RESULT 9  
ID KEFF\_SALTY STANDARD; PRT; 176 AA.  
AC Q829K1;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Glutathione-regulated potassium-efflux system ancillary protein keff.  
GN KEFF OR STY0100 OR T0088.  
OS Salmonella typhi.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Salmonella.  
OX NCBI\_TaxID=601;  
[1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=CT18;  
RX MEDLINE=21534947; PubMed=11677608;  
RA Churchill J., Dougan G., James K.D., Holden M.T.G., Sebithia M.,  
RA Churcher S., Mungall K.L., Bentley S.D., Holden M.T.G., Seabright M.,  
RA Baker S., Basham D., Brooks K., Chillingworth T., Cornerton P.,  
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,  
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,  
RA Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
RA Whitehead S., Barrett B.G.;  
RT "Complete genome sequence of a multiple drug resistant Salmonella  
RT enterica serovar Typhi CT18.";  
RL Nature 413:848-852(2001).  
[2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=Ty2 / ATCC 700931;  
RX MEDLINE=22531367; PubMed=12644504;  
RA Deng W., Liu S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,  
RA Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.;  
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2  
RT and CT18.";  
RL J. Bacteriol. 185:2330-2337(2003).  
CC -!- FUNCTION: Required for full activity of keff (By similarity).  
CC -!- MISCELLANEOUS: It is unlikely that keff has oxidoreductase  
CC activity, it has probably evolved from its function as  
CC oxidoreductase to be regulator of keff.  
CC -!- SIMILARITY: Belongs to the NAD(P)H dehydrogenase (quinone) family.  
CC Keff subfamily.

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CC -----  
DR EMBL, AL627265: CAD01241.1; -  
DR EMBL, AE016834: AAC67821.1; -  
DR HAMAP, MF\_01414: -; 1.  
DR InterPro, IPR003680: NADHdh\_2.  
DR Pfam, PF02525: Flavodoxin\_2; 1.  
DR Complete proteome.  
KM SEQUENCE 176 AA; 19943 MW; EC7627FB7B698027 CRC64;  
  
Query Match 60.9%; Score 39; DB 1; Length 176;  
Best Local Similarity 58.3%; Pred. No. 13;  
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;  
  
QY 1 WYD--PLTKLWL 10  
DB 67 WYSVPLTKLWL 78  
  
RESULT 10  
ID KEFF\_SALTY STANDARD; PRT; 176 AA.  
AC Q829K3;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Glutathione-regulated potassium-efflux system ancillary protein keff.  
GN KEFF OR STY0085.  
OS Salmonella typhimurium.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Salmonella.  
OX NCBI\_TaxID=602;  
[1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=L72 / SGSC1412 / ATCC 700720;  
RX MEDLINE=21534948; PubMed=11677609;  
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
RA Courtney L., Portolillo S., All U., Dante M., Du F., Hou S., Layman D.,  
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
RA Ryan B., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
RA Waterston R., Wilson R.K.;  
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium  
RT L72.";  
RL Nature 413:852-856(2001).  
CC -!- FUNCTION: Required for full activity of keff (By similarity).  
CC -!- MISCELLANEOUS: It is unlikely that keff has oxidoreductase  
CC activity, it has probably evolved from its function as  
CC oxidoreductase to be regulator of keff.  
CC -!- SIMILARITY: Belongs to the NAD(P)H dehydrogenase (quinone) family.  
CC Keff subfamily.  
CC -----  
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CC -----  
DR EMBL, AE008697: AAL19049.1; -  
DR StGene, SG77777; keff.  
DR HAMAP, MF\_01414: -; 1.  
DR InterPro, IPR003680: NADHdh\_2.  
DR Pfam, PF02525: Flavodoxin\_2; 1.  
KM Complete proteome.  
SQ SEQUENCE 176 AA; 20005 MW; 9B5CF2FB7B684B55 CRC64;



Query Match 60.9%; Score 39; DB 1; Length 176;  
Best Local Similarity 58.3%; Pred. No. 13;  
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 WYD--PLTKLWL 10  
DB 67 WYSVPLTKLMM 78

## RESULT 11

KEFP\_SHIFL STANDARD; PRT; 176 AA.

AC 083SQ4;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DE Glutathione-regulated potassium-efflux system ancillary protein kefp.  
GN KEFP OR SF0043 OR S0045.  
OS Shigella flexneri.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Shigella.  
OX NCBI\_TaxID=623.

RP SEQUENCE FROM N.A.  
RC STRAIN=301 / Serotype 2a;  
RX MEDLINE=22272406; PubMed=12384590;  
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,  
Yan J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,  
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,  
Cheng H., Tao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,  
Yu J.;  
RT "genome sequence of Shigella flexneri 2a: insights into pathogenicity  
through comparison with genomes of Escherichia coli K12 and O157.";  
RL Nucleic Acids Res. 30:4432-4441(2002).  
RN [2]

RP SEQUENCE FROM N.A.  
RC STRAIN=2457T / ATCC 700930 / Serotype 2a;  
RX MEDLINE=22590274; PubMed=12704152;  
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,  
Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,  
Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.D., Zhou S.,  
Schwartz D.C., Blattner F.R.;  
RT "Complete genome sequence and comparative genomics of Shigella  
flexneri serotype 2a strain 2457T.";  
RL Infect. Immun. 71:2775-2786(2003).  
RN [1]

CC -1- FUNCTION: Required for full activity of kefc (By similarity).  
CC -1- MISCELLANEOUS: It is unlikely that kefp has oxidoreductase  
CC activity, it has probably evolved from its function as  
CC oxidoreductase to be regulator of kefc.  
CC -1- SIMILARITY: Belongs to the NAD(P)H dehydrogenase (quinone) family.  
CC Kefp subfamily.

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DR EMBL; AE015041; AAN41709.1; -;  
DR EMBL; AE016978; AAP15589.1; -;  
DR HAMAP; MF\_01414; -; 1.  
DR InterPro; IPR003680; NADPH\_2.  
DR Pfam; PF02525; Flavodoxin\_2; 1.  
KW Complete proteome.

SEQUENCE 176 AA; 20336 MW; P84F037B2FAF6B CRC64;

Query Match 60.9%; Score 39; DB 1; Length 176;  
Best Local Similarity 58.3%; Pred. No. 13;  
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 WYD--PLTKLWL 10  
DB 67 WYSVPLTKLMM 78

## RESULT 12

KEFP\_KLEAE STANDARD; PRT; 177 AA.

AC 09X755;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DE Glutathione-regulated potassium-efflux system ancillary protein kefp.  
GN KEFP.  
OS Klebsiella aerogenes.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Klebsiella.  
OX NCBI\_TaxID=28451.  
RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=20507830; PubMed=11053405;  
RA Miller S., Ness L.S., Wood C.M., Fox B.C., Booth I.R.;  
RT "Identification of an ancillary protein, Yabp, required for activity  
of the Kefc glutathione-gated potassium efflux system in Escherichia  
coli";  
RL J. Bacteriol. 182:6536-6540(2000).  
CC -1- FUNCTION: Required for full activity of kefc (By similarity).  
CC -1- MISCELLANEOUS: It is unlikely that kefp has oxidoreductase  
CC activity, it has probably evolved from its function as  
CC oxidoreductase to be regulator of kefc.  
CC -1- SIMILARITY: Belongs to the NAD(P)H dehydrogenase (quinone) family.  
CC Kefp subfamily.

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DR EMBL; AJ242913; CAB44436.1; -;  
DR HSSP; P16083; IQR2.  
DR HAMAP; MF\_01414; -; 1.  
DR InterPro; IPR003680; NADPH\_2.  
DR Pfam; PF02525; Flavodoxin\_2; 1.  
SEQUENCE 177 AA; 20161 MW; 2D6457C4BBD7D39 CRC64;

Query Match 60.9%; Score 39; DB 1; Length 177;  
Best Local Similarity 58.3%; Pred. No. 13;  
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 WYD--PLTKLWL 10  
DB 67 WYSVPLTKLMM 78

## RESULT 13

BE1L\_SFV1 STANDARD; PRT; 308 AA.

AC P29169;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 01-JUL-1993 (Rel. 26, Last annotation update)  
DE BE1-1 protein.  
GN BE1-1 OR 1AF.  
OS Simian foamy virus (type 1) (SFV-1).  
OC Viruses; Retroviral viruses; Retroviridae; Spumavirinae.

OX NCBI\_TaxID=11964;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91276270; PubMed=1647358;  
Kupiec J.-C., Kay A., Hayat M., Peries J., Galibert F.;



RT "Sequence analysis of the simian foamy virus type 1 genome."  
 RL Gene 101:185-194(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91237804; PubMed=1851862;  
 RA Merz A., Shaw K.E.S., Pratt-Lowe E., Barry P.A., Luciw P.A.;  
 RT "Identification of the simian foamy virus transcriptional  
 RT transactivator gene (taf)."  
 RL J. Virol. 65:2903-2909(1991).  
 CC -1- FUNCTION: This protein is a transcriptional transactivator.  
 CC -----  
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 CC -----  
 CC EMBL, X54482; -; NOT ANNOTATED\_CDS.  
 DR EMBL, M74039; AAA47802.1; -.  
 DR PIR, B39924; WMLJ51.  
 DR PIR, S18740; S18740.  
 DR InterPro: IPR004956; Foamy BEL.  
 DR Pfam: PF03274; Foamy BEL; 1.  
 DR Transcription regulation; Activator.  
 KW CONFLICT 89 89 D -> N (IN REF. 2).  
 FT CONFLICT 119 119 D -> N (IN REF. 2).  
 FT CONFLICT 257 257 S -> G (IN REF. 2).  
 SQ SEQUENCE 308 AA; 35311 MW; 7E280B6EFB21D992 CRC64;

Query Match 60.9%; Score 39; DB 1; Length 308;  
 Best Local Similarity 66.7%; Pred. No. 22;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YDPLTKLW 10  
 DB 155 YDPELWV 163

RESULT 14  
 YASD MYCSM STANDARD; PRT; 333 AA.  
 AC P41602;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical 35.9 kDa protein in asd 3'region (ORFV).  
 OS Mycobacterium smegmatis.  
 OC Bacteria; Actinobacteria; Actinomycetales;  
 OC Corynebacteriidae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1772;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 607 / mc(2)6 / NRRL B-692;  
 RX MEDLINE=94254720; PubMed=7910936;  
 RA Citrillo J.D., Weisbrod T.R., Pascoeella L., Bloom B.R.,  
 RA Jacobs W.R. Jr.;  
 RT "Isolation and characterization of the aspartokinase and aspartate  
 RT semialdehyde dehydrogenase operon from mycobacteria";  
 RL Mol. Microbiol. 11:629-639(1994).  
 CC -----  
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 CC -----  
 CC EMBL, Z17372; CAA78987.1; -.  
 DR EMBL, Z17372; CAA78987.1; -.  
 DR PIR, S42424; S42424.  
 KW Hypothetical protein.

SQ SEQUENCE 333 AA; 35881 MW; C1C50D9A6DC37368 CRC64;  
 Query Match 60.9%; Score 39; DB 1; Length 333;  
 Best Local Similarity 66.7%; Pred. No. 24;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9  
 DB 209 WGDPAALW 217

RESULT 15  
 G6PD RHIME STANDARD; PRT; 491 AA.  
 AC Q9Z352;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (G6PD).  
 GN ZMF OR R00704 OR SMC03070.  
 OS Rhizobium meliloti (Sinorhizobium meliloti).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.  
 OX NCBI\_TaxID=382;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99328961; PubMed=10400573;  
 RA Willis L.B., Walker G.C.;  
 RT "A novel Sinorhizobium meliloti operon encodes an alpha-glucosidase  
 RT and a periplasmic-binding-protein-dependent transport system for  
 RT alpha-glucosides";  
 RL J. Bacteriol. 181:4176-4184(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1021;  
 RX MEDLINE=21396507; PubMed=11481430;  
 RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,  
 RA Bolstad F., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,  
 RA Godle T., Goffeau A., Kahn D., Kiss E., Lelaire V., Maury D.,  
 RA Pohl T., Portetelle D., Puehler A., Purnelle B., Rampeger U.,  
 RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;  
 RT "Analysis of the chromosome sequence of the legume symbiont  
 RT Sinorhizobium meliloti strain 1021";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
 CC -1- CATALYTIC ACTIVITY: D-glucose 6-phosphate + NADP(+) = D-glucono-  
 CC -1- 5-lactone 6-phosphate + NADPH.  
 CC -1- PATHWAY: Pentose phosphate pathway; first step.  
 CC -1- SIMILARITY: Belongs to the glucose-6-phosphate dehydrogenase  
 CC family.  
 CC -----  
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 CC -----  
 CC EMBL, AF045609; AAD12043.1; -.  
 DR EMBL, AF045609; AAD12043.1; -.  
 DR HSSP; P11411; 10PG  
 DR InterPro: IPR001282; G6PD.  
 DR Pfam: PF00479; G6PD; 1.  
 DR Pfam: PF02781; G6PD; 1.  
 DR PRINTS; PR00079; G6PDHRCNASE.  
 DR PRODOM; PD001129; G6PDHRCNASE.  
 DR TIGRPMs; TIGR00871; zwf; 1.  
 DR PROSITE; PS00069; G6P\_DEHYDROGENASE; 1.  
 KW Oxidoreductase; NADP; Glucose metabolism; Complete proteome.  
 KM ACT SITE 184 184 R -> T (IN REF. 1).  
 FT CONFLICT 401 401 R -> T (IN REF. 1).  
 SQ SEQUENCE 491 AA; 55301 MW; 0D8B1AFD094E1775 CRC64;

Query Match 60.9%; Score 39; DB 1; Length 491;  
Best Local Similarity 55.6%; Pred. No. 36;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WDPJTKLM 9  
DB 448 WDPJTKLM 456

RESULT 16  
Y644\_MYCLB  
ID Y644\_MYCLB STANDARD; PRT; 983 AA.  
AC Q9CCM6; O32904;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DE 15-MAR-2004 (Rel. 43, Last annotation update)  
GN ML0644 OR MLCB1779.46.  
OS Mycobacterium leprae.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxId=1769;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TN;  
RX MEDLINE=21128732; PubMed=11234002;  
RA Cole S.T., Eiglmier K., Parkhill J., James K.D., Thomson N.R.,  
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,  
RA Duggill K., Basham D., Brown D., Chillingworth T., Connor R.,  
RA Davies R.M., Devlin K., Doherty S., Feltwell T., Fraser A., Hamlin N.,  
RA Holtroyd S., Hornby T., Jagels K., Lacroix C., Maclean J., Moule S.,  
RA Murphy L., Oliver K., Quail M.A., Rajadream M.A., Rutherford K.M.,  
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,  
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,  
RA Barrell B.G.;  
RT "Massive gene decay in the leprosy bacillus.";  
RL Nature 409:1007-1011(2001).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -1- SIMILARITY: Belongs to the UPF0182 family.

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CC EMBL; AL583919; CAC30153.1; -  
CC EMBL; Z98271; CAB11027.1; ALT\_INIT.  
CC PIR; E86989; E86989.  
CC Leptoma; ML0644; -  
CC HAMAP; MF\_01600; -; 1.  
DR InterPro; IPR005372; UPF0182.  
DR Pfam; PF03699; UPF0182; 1.  
KW Hypothetical protein; Transmembrane; Complete proteome.

FT TRANSMEM 20 37 POTENTIAL.  
FT TRANSMEM 63 85 POTENTIAL.  
FT TRANSMEM 113 135 POTENTIAL.  
FT TRANSMEM 169 191 POTENTIAL.  
FT TRANSMEM 212 229 POTENTIAL.  
FT TRANSMEM 260 277 POTENTIAL.  
FT TRANSMEM 284 306 POTENTIAL.  
SQ SEQUENCE 983 AA; 107556 MW; BC8AA30433CA594F CRC64;

Query Match 60.9%; Score 39; DB 1; Length 983;  
Best Local Similarity 55.6%; Pred. No. 73;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 YDPJTKLM 10  
DB 666 YDPJTKLM 674

RESULT 17  
CINA\_HUMAN STANDARD; PRT; 538 AA.  
ID CINA\_HUMAN  
AC P57789; Q8TDK7; Q8TDK8; Q9HB59;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE 15-MAR-2004 (Rel. 43, Last annotation update)  
GN Potassium channel subfamily K member 10 (Outward rectifying potassium  
DB channel protein TREK-2) (TREK-2 K+ channel subunit).  
GN KCNK10 OR TREK2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM A).  
RX MEDLINE=20435789; PubMed=10880510;  
RA Lesage F., Terrenoire C., Romey G., Lazdunski M.;  
RT "Human TREK2, a 2P domain mechano-sensitive K+ channel with multiple  
RT regulations by polyunsaturated fatty acids, lysophospholipids and Gs,  
RT G1, and Gq protein-coupled receptors.";  
RL J. Biol. Chem. 275:28398-28405(2000).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS B AND C).  
RX MEDLINE=21896087; PubMed=11897838;  
RA Gu W., Schlichter G., Hirsch J.R., Engels H., Karschin C.,  
RA Karschin A., Destr C., Steinlein O.K., Daut J.;  
RT "Expression pattern and functional characteristics of two novel splice  
RT variants of the two-pore-domain potassium channel TREK-2.";  
RL J. Physiol. (Lond) 539:657-668(2002).  
CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL. PRODUCES RAPIDLY  
CC ACTIVATING AND NON-INACTIVATING OUTWARD RECTIFIER K(+) CURRENTS.  
CC UNSATURATED FREE FATTY ACIDS.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -1- ALTERNATIVE PRODUCTS:  
CC Name=A; Synonyms=TREK-2a;  
CC IsoId=P57789-1; Sequence=Displayed;  
CC Name=B; Synonyms=TREK-2b;  
CC IsoId=P57789-2; Sequence=VSP\_006697;  
CC Name=C; Synonyms=TREK-2c;  
CC IsoId=P57789-3; Sequence=VSP\_006698;  
CC -1- TISSUE SPECIFICITY: Abundantly expressed in pancreas and kidney  
CC and to a lower level in brain, testis, colon, and small intestine.  
CC Isoform b is strongly expressed in kidney (primarily in the  
CC proximal tubule) and pancreas, whereas isoform c is abundantly  
CC expressed in brain.  
CC -1- SIMILARITY: Belongs to the two pore domain potassium channel  
CC family.

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CC EMBL; AF279890; AAC15191.1; -  
CC EMBL; AF385399; AAL95705.1; -  
CC EMBL; AF385400; AAL95706.1; -  
CC Genew; HGNC:6273; KCNK10.  
CC MIM; 605873; -  
DR GO; GO:0005267; F:potassium channel activity; TAS.  
DR GO; GO:0006810; P:transport; TAS.  
DR InterPro; IPR003280; K+channel\_2pore.  
DR InterPro; IPR001622; K+channel\_pore.  
DR InterPro; IPR003976; Trek\_channel.  
DR PRINTS; PR01333; 2PORKCHANNEL.  
DR PRINTS; PR01499; TREKCHANNEL.  
KW Transport; Ion transport; Ionic channel; Voltage-gated channel;

Potassium channel; Potassium; Transmembrane; Glycoprotein;  
KW Alternate splicing: 71  
FT DOMAIN 1 71 CYTOPLASMIC (POTENTIAL).  
FT TRANSSEM 72 92 POTENTIAL.  
FT DOMAIN 154 180 PORE-FORMING 1 (POTENTIAL).  
FT TRANSSEM 182 202 POTENTIAL.  
FT DOMAIN 203 233 CYTOPLASMIC (POTENTIAL).  
FT TRANSSEM 234 254 POTENTIAL.  
FT DOMAIN 263 294 PORE-FORMING 2 (POTENTIAL).  
FT TRANSSEM 299 319 POTENTIAL.  
FT DOMAIN 320 538 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VAAPSLIC 1 12 MFFLYTDFPLSL -> MGDRTGCRSDS (in isoform B).  
FT VAAPSLIC 1 12 /FTID=VSP\_006697.  
FT VAAPSLIC 1 12 MFFLYTDFPLSL -> MFFPIETPRKQVNDPK (in isoform C).  
FT VAAPSLIC 1 12 /FTID=VSP\_006698.  
FT VAAPSLIC 1 12 E -> G (IN REF. 2).  
FT VAAPSLIC 1 12 /FTID=VSP\_006698.  
FT VAAPSLIC 1 12 E -> G (IN REF. 2).  
SQ SEQUENCE 538 AA; 59764 MW; 8EA615B08D147FBC CRC64;  
Query Match 59.4%; Score 38; DB 1; Length 538;  
Best Local Similarity 50.0%; Pred. No. 58;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
OY 1 WYDPLTKLML 10  
DB 295 WYKPLWFWMI 304  
RESULT 18  
C1WA\_RAT STANDARD; PRT; 538 AA.  
ID C1WA\_RAT  
AC 09JIS4;  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Potassium channel subfamily K member 10 (Outward rectifying potassium channel protein TREK-2) (TREK-2 K+ channel subunit).  
GN KCNK10 OR TREK2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10116;  
RN SEQUENCE FROM N.A.  
RX MEDLINE=20298807; PubMed=10747911;  
RA Bang H., Kim Y., Kim D.  
RT "TREK-2, a new member of the mechanosensitive tandem-pore K+ channel family.";  
RT J. Biol. Chem. 275:17412-17419(2000).  
CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL. PRODUCES RAPIDLY ACTIVATING AND NON-INACTIVATING OUTWARD RECTIFIER K(+) CURRENTS. ACTIVATED BY ARACHIDONIC ACID AND OTHER NATURALLY OCCURRING UNSATURATED FREE FATTY ACIDS.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -1- TISSUE SPECIFICITY: EXPRESSED MAINLY IN THE CEREBELLUM, SPLEEN, AND TESTIS.  
CC -1- SIMILARITY: Belongs to the two pore domain potassium channel family.  
-----  
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CC EMBL; AF196965; AAF75132.1; -  
DR InterPro; IPR003280; K+channel\_2pore.

InterPro; IPR001622; K+channel\_pore.  
DR InterPro; IPR003976; Trek channel.  
DR PRINTS; PR01333; 2PORECHANNEL.  
DR PRINTS; PR01499; TREKCHANNEL.  
KW Transport; Ion transport; Ionic channel; Voltage-gated channel; Potassium channel; Potassium; Transmembrane; Glycoprotein.  
FT DOMAIN 1 71 CYTOPLASMIC (POTENTIAL).  
FT TRANSSEM 72 92 POTENTIAL.  
FT DOMAIN 154 180 PORE-FORMING 1 (POTENTIAL).  
FT TRANSSEM 182 202 POTENTIAL.  
FT DOMAIN 203 233 CYTOPLASMIC (POTENTIAL).  
FT TRANSSEM 234 254 POTENTIAL.  
FT DOMAIN 263 294 PORE-FORMING 2 (POTENTIAL).  
FT TRANSSEM 299 319 POTENTIAL.  
FT DOMAIN 320 538 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 538 AA; 59800 MW; 1FF33F0AA5289784 CRC64;  
Query Match 59.4%; Score 38; DB 1; Length 538;  
Best Local Similarity 50.0%; Pred. No. 58;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
OY 1 WYDPLTKLML 10  
DB 295 WYKPLWFWMI 304  
RESULT 19  
METH SYN3 STANDARD; PRT; 1195 AA.  
ID METH SYN3  
AC 055786;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE 5-methyltetrahydrofolate-homocysteine methyltransferase (EC 2.1.1.13) (Methionine synthase, vitamin-B12 dependent isozyme) (MS).  
GN METH OR SUR0212.  
OS Synchocystis sp. (strain PCC 6803).  
OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.  
OX NCBI\_TaxID=1148;  
RN SEQUENCE FROM N.A.  
RX MEDLINE=9612752; PubMed=8590279;  
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N., Sugita M., Tabata S.;  
RT "Sequence analysis of the genome of the unicellular cyanobacterium Synchocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64k to 92k of the genome.";  
RL DNA Res. 2:153-166(1995).  
CC -1- CATALYTIC ACTIVITY: 5-methyltetrahydrofolate + L-homocysteine = tetrahydrofolate + L-methionine.  
CC -1- COFACTOR: Cobalamin (By similarity).  
CC -1- PATHWAY: Terminal step in the de novo biosynthesis of methionine.  
CC -1- SIMILARITY: Belongs to the vitamin-B12 dependent methionine synthase family.  
-----  
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CC EMBL; D64002; BAA10438.1; -  
DR PIR; S76592; S76592.  
DR HSP; P13009; 1BMT.  
DR InterPro; IPR006158; B12-binding.  
DR InterPro; IPR003759; Cofet\_synth\_B12.  
DR InterPro; IPR000489; Dhdropt\_synth.  
DR InterPro; IPR004223; Met\_synth\_B12.  
DR InterPro; IPR003726; S\_methyl\_trans.

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DR Pfam: PF02310; B12-binding; 1.
DR Pfam: PF02607; B12-binding; 2; 1.
DR Pfam: PF02965; Met_synth_B12; 1.
DR Pfam: PF00809; Pterin_bind; 1.
DR Pfam: PF02574; S-methyl_trans; 1.
DR Transferrase; Methyltransferase; Methionine biosynthesis; Vitamin B12;
KW Cofact; Complete proteome.
FT DOMAIN 735 812 COBLAMIN-BINDING (POTENTIAL).
FT METAL 737 737 COBLMT (POTENTIAL).
SQ SEQUENCE 1195 AA; 132539 MW; 1D9635B1BD583 CRC64;

Query Match 59.4%; Score 38; DB 1; Length 1195;
Best Local Similarity 100.0%; Pred. No. 1,3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 2 YDPLTKL 8
Db 611 YDPLTKL 617

RESULT 20
YLK3 CAEEL STANDARD; PRT; 1576 AA.
AC P41951; Q950P7;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative serine/threonine-protein kinase D1044.3 in chromosome III
GN (PC 2.7.1.-).
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCB1_TaxID=6239;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=Briscel N2;
RA Pauley A.; Waterston R.;
RN Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
[2]
RP REVISIONS, AND ALTERNATIVE SPLICING.
RA Waterston R.;
RN Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
-1- ALTERNATIVE PRODUCTS;
Event=Alternative splicing; Named isoforms=2;
Name=a;
Isoid=P41951-1; Sequence=Displayed;
Name=b;
Isoid=P41951-2; Sequence=VSP 004900, VSP 004901;
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
STRONG, TO ZC64.1.
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CC EMBL; U00065; AAK68286.1; -.
CC EMBL; U00065; AAL27237.1; -.
CC HSSP; Q63450; 1A06
CC WormRep; D1044.3b; CE27894.
CC WormRep; D1044.3b; CE29743.
CC InterPro; IPR008938; ARM.
CC InterPro; IPR006149; EB_region.
CC InterPro; IPR008271; Ser_thr_kinase.
CC InterPro; IPR002290; Ser_thr_kinase.
CC InterPro; IPR006150; Worm_repeat_1.
CC Pfam; PF01683; EB; 8.
CC Pfam; PF00069; Pkinase; 1.

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DR	Prodom	P00000001; Prot_kinase; 1.
DR	SMART	SM00220; S_TKc_1.
DR	SMART	SM00289; Mtl_8.
DR	PROSITE	PS00107; PROTEIN KINASE_ATP; 1.
DR	PROSITE	PS00108; PROTEIN KINASE_ST; 1.
DR	PROSITE	PS0011; PROTEIN_KINASE_DOM; 1.
KW	Hypothetical protein; Transferase; Serine/threonine-protein kinase;	
KM	ATP-binding; Alternative splicing.	
FT	DOMAIN	431 .. 703
FT	NP_BIND	437 .. 445
FT	BINDING	461 .. 461
FT	ACT_SITE	569 .. 569
FT	VARSPLIC	1 .. 904
FT	FT	
FT	FT	
FT	VARSPLIC	905 .. 1012
SQ	SEQUENCE	1576 AA; 174677 MW; 3A1EE573EBD13498 CRC64; /FtId=VSP_004901. /FtId=VSP_004901.
Qy	Query Match	59.4%; Score 38; DB 1; Length 1576; Best Local Similarity 62.5%; Pred. No. 1.7e+02; Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0
Db	2 YDPPLTKLM 9     : 659 YDPLNEMW 666	
RESULT 21	DAPA_COREF	STANDARD; PRT; 301 AA.
ID	DAPA_COREF	
AC	O8R0M8;	
DT	28-FEB-2003 (Rel. 41, Created)	
DT	28-FEB-2003 (Rel. 41, Last sequence update)	
DT	10-OCT-2003 (Rel. 42, Last annotation update)	
DE	dihydrodipicolinate synthase [EC 4.2.1.52] (DHDDS).	
DS	DAPA OR CE1864.	
OS	Corynebacterium efficiens.	
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;	
OC	Corynebacterales; Corynebacteriaceae; Corynebacterium.	
OX	NCB1_TaxID=152794;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;	
RA	Itoya H., Kimura E., Kawahara Y., Sugimoto S.;	
RT	"dapB, dapa of Corynebacterium efficiens."	
RL	Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;	
RA	MEDLINE=2273752; PubMed=12840036;	
RX	Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,	
RA	Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,	
RA	Gojohori T.;	
RT	"Comparative complete genome sequence analysis of the amino acid	
RT	replacements responsible for the thermostability of Corynebacterium	
RT	efficiens.";	
RL	Genome Res. 13:1572-1579 (2003).	
CC	-1- CATALYTIC ACTIVITY: L-aspartate 4-semialdehyde + pyruvate =	
CC	dihydrodipicolinate + 2 H(2)O.	
CC	-1- PATHWAY: Biosynthesis of diaminopimelate and lysine from aspartate	
CC	semialdehyde; first step.	
CC	-1- SUBUNIT: Homotrimer (By similarity).	
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).	
CC	-1- SIMILARITY: Belongs to the DHDS family.	
CC	-----	
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CC -----
DR EMBL: AB083130; BAB88823.1; -
DR EMBL: AP005220; BAC18674.1; ALT_INIT.
DR HAMAP: MF_00418; -; 1.
DR InterPro: IPR005263; DADA.
DR Pfam: PF00701; DHDPs_1.
DR PRINTS: PR00146; DHPICNTHASE.
DR PRODOM: PD001859; DHDPs_1.
DR TIGRFAMs: TIGR00674; dapa; 1.
DR PROSITE: PS00665; DHDPs_1; 1.
DR PROSITE: PS00666; DHDPs_2; 1.
KW Lyase; Diaminopimelate biosynthesis; lysine biosynthesis;
KW Complete proteome.
FT ACT_SITE 173
SQ SEQUENCE 301 AA; 31450 MW; D48FC57E4F00AFA CRC64;

Query Match 58.6%; Score 37.5; DB 1; Length 301;
Best Local Similarity 53.8%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

OY 1 WY---DPLTKLWL 10
DB 193 WYSGDDPLNLVWL 205

RESULT 22
DADA CORGL STANDARD; PRT; 301 AA.
ID DADA CORGL STANDARD; PRT; 301 AA.
AC P19808; P40109;
DT 01-FEB-1991 (Rel. 17, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydrodipicolinate synthase (EC 4.2.1.52) (DHDPs).
GN DADA OR CGL1971.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13059 / AS019;
RX MEDLINE=91057127; PubMed=2129555;
RA Bonnasie S.; Oreglia J.; Sicard A.M.;
RT "Nucleotide sequence of the dapa gene from Corynebacterium
RT glutamicum."
RL Nucleic Acids Res. 18:6421-6421 (1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13869;
RX MEDLINE=93239702; PubMed=8478336;
RA Piabarro A.; Malumbres M.; Mateos L.M.; Oguiza J.A.; Martin J.F.;
RT "A cluster of three genes (dapa, orf2, and daps) of Brevibacterium
RT lactofermentum encodes dihydrodipicolinate synthase,
RT dihydrodipicolinate reductase, and a third polypeptide of unknown
RT function."
RL J. Bacteriol. 175:2743-2749 (1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RX "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: L-aspartate 4-semialdehyde + pyruvate =
CC dihydrodipicolinate + 2 H(2)O.
CC -1- PATHWAY: Biosynthesis of diaminopimelate and lysine from aspartate
CC semialdehyde; first step.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
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CC -1- SIMILARITY: Belongs to the DHDPs family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X53993; CA37940.1; -
DR EMBL: Z21502; CA479714.1; -
DR EMBL: AP005280; BAB99364.1; -
DR PIR: C40626; C40626.
DR HSSP: P05640; IDHP.
DR HAMAP: MF_00418; -; 1.
DR InterPro: IPR005263; DADA.
DR InterPro: IPR002220; DHDPs.
DR Pfam: PF00701; DHDPs_1.
DR PRINTS: PR00146; DHPICNTHASE.
DR PRODOM: PD001859; DHDPs_1.
DR TIGRFAMs: TIGR00674; dapa; 1.
DR PROSITE: PS00665; DHDPs_1; 1.
DR PROSITE: PS00666; DHDPs_2; 1.
KW Lyase; Diaminopimelate biosynthesis; lysine biosynthesis;
KW Complete proteome.
FT ACT_SITE 173
FT CONFICT 266
SQ SEQUENCE 301 AA; 31261 MW; 6B803A4E82933B3 CRC64;

Query Match 58.6%; Score 37.5; DB 1; Length 301;
Best Local Similarity 53.8%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

OY 1 WY---DPLTKLWL 10
DB 193 WYSGDDPLNLVWL 205

RESULT 23
XY12 CAEEL STANDARD; PRT; 316 AA.
ID XY12 CAEEL STANDARD; PRT; 316 AA.
AC Q1123;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 35.1 kDa protein C03F11.2 in chromosome X.
GN C03F11.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabditoidea;
OC Rhabdilitidae; Pelodetrinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol NZ;
RA Bentley D.;
RT Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: WEAK, IN THE N-TERMINUS. TO C. ELIGANS F53B1.5.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U39744; AK18883.1; -
DR PIR: T15395; T15395.
DR WormPep: C03F11.2; C03F11.2.
DR InterPro: IPR001279; Blactamase-like.
DR Pfam: PF00753; lactamase_B; 1.
KW Hypothetical protein.
```

SQ SEQUENCE 316 AA; 35107 MM; 6A725FCAC21CF676 CRC64;  
 Query Match 57.8%; Score 37; DB 1; Length 316;  
 Best Local Similarity 66.7%; Pred. No. 50;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Oy 1 WYDPLTKLM 9  
 Db 301 WQTLTKLM 309

RESULT 24  
 ID MK32 YEAST STANDARD; PRT; 363 AA.  
 AC P23060;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE MAK32 protein.  
 GN MAK32 OR YCR019W OR YCR19W.  
 OS Saccharomyces cerevisiae (Baker's Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89131254; PubMed=3916862;  
 RA Toh-E A., Sahaishi Y.;  
 RT "The PER1 locus of *Saccharomyces cerevisiae*: a complex locus  
 RT containing multiple genes."  
 RL Yeast 1:159-171 (1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Feldmann H., Mannhaupt G., Vetter I.;  
 RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Necessary for the structural stability of U-A double-  
 CC stranded RNA-containing particles. Necessary for growth at 37  
 CC degrees Celsius as well as for maintenance of the killer plasmid.  
 CC -1- SIMILARITY: TO S.POMBE SPAC4G8.14C.  
 CC -----  
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 CC -----  
 CC DR EMBL; X59720; CAA42310.1; -  
 CC DR PIR; S19429; BVBYK2.  
 CC DR Germonline; 138924; -  
 CC DR SGD; S0000612; MAK32.  
 CC DR GO; GO:0019048; P:virus-host interaction; IMP.  
 CC FT CONFLICT 15 I -> II (IN REF. 1).  
 CC FT CONFLICT 82 MISSING (IN REF. 1).  
 CC SQ SEQUENCE 363 AA; 40783 MM; CFB358F8ACFEAC CRC64;

Query Match 57.8%; Score 37; DB 1; Length 363;  
 Best Local Similarity 62.5%; Pred. No. 57;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 Oy 2 YDPLTKLM 9  
 Db 325 YDPIAKTW 332

RESULT 25  
 ERG6 YEAST STANDARD; PRT; 392 AA.  
 AC P25087;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-OCT-1984 (Rel. 30, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Sterol 24-C-methyltransferase (EC 2.1.1.41) (Delta(24)-sterol C-  
 DE methyltransferase).  
 GN ERG6 OR SED6 OR ISE1 OR LIS1 OR YML008C OR YM9571.10C.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94262330; PubMed=8203167;  
 RA Hardwick K.G., Pelham H.R.B.;  
 RT "SED6 is identical to ERG6, and encodes a putative methyltransferase  
 RT required for ergosterol synthesis."  
 RL Yeast 10:265-269 (1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94312403; PubMed=8038180;  
 RA Weljhind A.A., Beavis A.D., Trumbly R.J.;  
 RT "Mutations in *LIS1* (ERG6) gene confer increased sodium and lithium  
 RT uptake in *Saccharomyces cerevisiae*."  
 RL Biochim. Biophys. Acta 1193:107-117 (1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=5288C / AB972;  
 RX MEDLINE=97313268; PubMed=9169872;  
 RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,  
 RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,  
 RA Jagsels K., Iye G., Moule S., Odell C., Pearson D., Rajandream M.A.,  
 RA Rice P., Skelton J., Walsh S., Whitehead S., Barrett B.G.;  
 RT "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome  
 RT XII."  
 RL Nature 387:90-93 (1997).  
 RN [4]  
 RP SEQUENCE OF 1-257 FROM N.A.  
 RX MEDLINE=91285426; PubMed=2060792;  
 RA Hussain M., Leonard J.;  
 RT "Characterization of PDR4, a *Saccharomyces cerevisiae* gene that  
 RT confers pleiotropic drug resistance in high-copy number: identity  
 RT with YAP1, encoding a transcriptional activator."  
 RL Gene 101:149-152 (1991).  
 RN [5]  
 RP ACETYLATION.  
 RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,  
 RA Volpe T., Warner J.R., McLaughlin C.S.;  
 RL Submitted (SEP-1994) to Swiss-Prot.  
 CC -1- FUNCTION: Methyltransferase required for ergosterol synthesis.  
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 5-alpha-cholest-  
 CC 8,24-dien-3-beta-ol = S-adenosyl-L-homocysteine + 24-methylene-5-  
 CC alpha-cholest-8-en-3-beta-ol.  
 CC -----  
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 CC -----  
 CC DR EMBL; X74249; CAA52308.1; -  
 CC DR EMBL; 572460; AAB31378.1; -  
 CC DR EMBL; 249810; CAA89944.1; -  
 CC DR EMBL; X53830; CAA37826.1; -  
 CC DR PIR; S42003; S42003.  
 CC DR Germonline; 142538; -  
 CC DR SWISS-2DPAGE; P25087; YEAST.  
 CC DR SGD; S0004467; ERG6.  
 CC DR GO; GO:0005811; C:lipid particle; IDA.  
 CC DR InterPro; IPR001601; Methyltransf.  
 CC DR InterPro; IPR000051; SAM bind.  
 CC KW Sterol biosynthesis; Transferase; Methyltransferase; Acetylation.  
 CC FT INIT MET 0  
 CC FT MOD RES 1 0  
 CC FT CONFLICT 379 379 ACETYLATION.  
 CC E -> EE (IN REF. 2).

SQ SEQUENCE 382 AA; 43299 MW; D76BA9E3D9CD71B CRC64;  
 Query Match 57.8%; Score 37; DB 1; Length 382;  
 Best Local Similarity 66.7%; Pred. No. 60;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 WYDPLTKLM 9  
 Db 285 WYDPLTKLM 293

RESULT 26  
 YB64 SCHPO STANDARD; PRT; 384 AA.  
 ID YB64 SCHPO  
 AC 009745; 1-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypothetical protein C12C2.04 in chromosome II.  
 GN SPIC12C2.04.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OC NCBI\_TaxID=4896;  
 [1]  
 SEQUENCE FROM N.A.  
 RP STRAIN=972;  
 RC MEDLINE=21848401; PubMed=11859360;  
 RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holtz S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,  
 RA James K., Jones L., Jones M., Leacher S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch B.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volkart G., Aert R., Robben J., Grymoprez B.,  
 RA Welter J., Vanterre E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Meesl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Wedler H., Wambolt R., Punnett B.,  
 RA Goffeau A., Cadieu B., Dreano S., Gloux S., Lelaire V., Motier S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
 RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;  
 RT "The genome sequence of Schizosaccharomyces pombe";  
 RL Nature 415:871-880(2002).  
 CC -1- SIMILARITY: TO S.POMBE SPAC2B1.17.  
 CC  
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 CC  
 CC EMBL; Z54140; CAA90817.1; -  
 DR PIR; T39377; T39377.  
 DR GenBank; SPBC12C2.04; -  
 KW Hypothetical protein.  
 SO SEQUENCE 384 AA; 43031 MW; 3DB5A4D615098C98 CRC64;

Query Match 57.8%; Score 37; DB 1; Length 384;  
 Best Local Similarity 75.0%; Pred. No. 60;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 1 WYDPLTKL 8  
 Db 247 WYDPCGRL 254

RESULT 27  
 CARA ANASP STANDARD; PRT; 388 AA.  
 ID CARA ANASP  
 AC 08YX07;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Carbamoyl-phosphate synthase small chain (EC 6.3.5.5) (Carbamoyl-  
 DE phosphate synthetase glutamine chain).  
 GN CARA OR ALR1155.  
 OS Anabaena sp. (strain PCC 7120).  
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
 OC NCBI\_TaxID=103690;  
 [1]  
 SEQUENCE FROM N.A.  
 RP MEDLINE=21595285; PubMed=11759840;  
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,  
 RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kohara M., Matsunoto M., Matsuno A., Muraki A.,  
 RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yanada M.,  
 RA Yaoda M., Tabata S.;  
 RT "Complete genomic sequence of the filamentous nitrogen-fixing  
 RT cyanobacterium Anabaena sp. strain PCC 7120.";  
 RL DNA Res. 8:205-213(2001).  
 CC -1- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP +  
 CC phosphate + L-glutamate + carbamoyl phosphate.  
 CC -1- PATHWAY: Arginine biosynthesis.  
 CC -1- PATHWAY: Pyrimidine biosynthesis; first step.  
 CC -1- SUBUNIT: Composed of two chains; the small (or glutamine) chain  
 CC promotes the hydrolysis of glutamine to ammonia, which is used by  
 CC the large (or ammonia) chain to synthesize carbamoyl phosphate (by  
 CC similarity).  
 CC -1- SIMILARITY: Belongs to the cara family.  
 CC -1- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.  
 CC  
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 CC  
 CC EMBL; AP003564; BAB73112.1; -  
 DR PIR; AH1950; AH1950.  
 DR HAMAP; MF\_01209; -; 1.  
 DR InterPro; IPR006274; CARA synth small.  
 DR InterPro; IPR001317; CP synthGATase.  
 DR InterPro; IPR002474; CP synthsmall.  
 DR InterPro; IPR000991; GATase\_1.  
 DR Pfam; PF00988; CPase\_sm chain; 1.  
 DR Pfam; PF00117; GATase\_1.  
 DR PRINTS; PR00099; CPsGATASE.  
 DR PRINTS; PR00096; GATASE.  
 DR TIGRFS; TIGR01368; CPsaseIsmall; 1.  
 DR PROSITE; PS00442; GATASE\_TYPE\_1; 1.  
 KW Arginine biosynthesis, Pyrimidine biosynthesis, ligase;  
 KW Glutamine amidotransferase; Complete proteome.  
 FT DOMAIN 1 192  
 FT ACT SITE 193 388  
 FT ACT SITE 272 272  
 SO SEQUENCE 388 AA; 42256 MW; 062A038D8F4B705E CRC64;

Query Match 57.8%; Score 37; DB 1; Length 388;  
 Best Local Similarity 55.6%; Pred. No. 61;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;



OY 1 WYDPLTKLM 9  
DB 173 WSDPTAVW 181

RESULT 28  
RP3A\_MOUSE  
ID RP3A\_MOUSE STANDARD; PRT; 681 AA.  
AC P47708;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Rabphilin-3A (Exophilin 1).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RA Itagaki N.;  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Brain, and Eye;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP SEQUENCE OF 1-606 FROM N.A.  
RC STRAIN=C57BL/6;  
RX MEDLINE=9512445; PubMed=7822236;  
RA Inagaki N., Mizuta M., Seino S.;  
RT "Cloning of a mouse Rabphilin-3A expressed in hormone-secreting cells.";  
RL J. Biochem. 116:239-242(1994).  
RN [4]  
RP FUNCTION: Protein transport. Probably involved with Ras-related protein Rab-3A in synaptic vesicle traffic and/or synaptic vesicle fusion. Could play a role in neurotransmitter release by regulating membrane flow in the nerve terminal.  
CC -1- SUBUNIT: Monomer.  
CC -1- TISSUE SPECIFICITY: Specifically expressed in brain.  
CC -1- SIMILARITY: Contains 1 FIVE-type zinc finger.  
CC -1- SIMILARITY: Contains 1 Rab-type domain.  
CC -1- SIMILARITY: Contains 1 Rab-binding (RabBD) domain.  
CC -----  
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CC EMBL: BC042585; AA042585.1; -  
DR EMBL: BC050883; AA050883.1; -  
DR EMBL: D29965; BA06231.2; -  
DR PIR: JX0338; JX0338.  
DR HSSP: P47709; 12BD.  
DR MGD: MGI:102788; Rph3a.  
DR GO: GO:0005515; F:protein binding; IPI.  
DR InterPro: IPR000008; C2.  
DR InterPro: IPR008973; C2\_CaLB.  
DR InterPro: IPR002149; LRT.  
DR InterPro: IPR003151; RPH3A\_effector.  
DR InterPro: IPR001565; Synaplocagmin.  
DR Pfam: PF00168; C2; 2.  
DR Pfam: PF02318; RPH3A\_effector; 1.  
DR PRINTS: PR00360; C2DOMAIN.  
DR PRINTS: PR00399; STNAPTOAGMN.  
DR SMART: SM00239; C2; 2.  
DR PROSITE: PS00499; C2\_DOMAIN\_1; 2.  
DR PROSITE: PS50004; C2\_DOMAIN\_2; 2.  
DR PROSITE: PS50916; RABBD; 1.  
DR PROSITE: PS50178; ZF\_FYVE; 1.  
KW Repeat, Synapse, Protein transport, Zinc-finger.  
FT DOMAIN 40 157 RAB-BINDING.  
FT ZN\_FING 88 145 FYVE-TYPE.  
FT DOMAIN 277 361 PRO-RICH.  
FT DOMAIN 381 485 C2\_DOMAIN\_1.  
FT DOMAIN 539 642 C2\_DOMAIN\_2.  
SQ SEQUENCE 681 AA; 75489 MM; D09F8DD2CBB271E CRC64;

Query Match 57.8%; Score 37; DB 1; Length 681;  
Best Local Similarity 75.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 DPLTKLML 10  
DB 574 DPEVKLML 581

RESULT 29  
RP3A\_RAT  
ID RP3A\_RAT STANDARD; PRT; 684 AA.  
AC P47709;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Rabphilin-3A (Exophilin 1).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9503210; PubMed=7946335;  
RA Li C., Takei K., Geppert M., Daniell L., Stenius K., Chapman E.R.,  
RA Jahn R., de Camilli P., Südhof T.C.;  
RT "Synaptic targeting of rabphilin-3A, a synaptic vesicle Ca2+/phospholipid-binding protein, depends on rab3A/3C.";  
RL Neuron 13:885-898(1994).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 44-167 IN COMPLEX WITH RAB3A.  
RC TISSUE=Brain;  
RX MEDLINE=99148269; PubMed=10025402;  
RA Ostermeier C., Brunger A.T.;  
RT "Structural basis of Rab effector specificity: crystal structure of the small G protein Rab3A complexed with the effector domain of rabphilin-3A.";  
RL Cell 96:363-374(1999).  
RN [3]  
RP FUNCTION: Protein transport. Probably involved with Ras-related protein Rab-3A in synaptic vesicle traffic and/or synaptic vesicle fusion. Could play a role in neurotransmitter release by



regulating membrane flow in the nerve terminal.

CC -1- SUBUNIT: Monomer.

CC -1- TISSUE SPECIFICITY: Specifically expressed in brain.

CC -1- SIMILARITY: Contains 2 C2 domains.

CC -1- SIMILARITY: Contains 1 FIVE-type zinc finger.

CC -1- SIMILARITY: Contains 1 Rab-binding (RabBD) domain.

CC -----

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CC -----

CC EMBL; U12571; AAA62662.1; -

CC PIR; I58166; I58166.

CC PDB; 1ZBD; 12-APR-99.

CC PDB; 3RBB; 23-DEC-99.

CC InterPro; IPR000008; C2.

CC InterPro; IPR008973; C2\_CaLB.

CC InterPro; IPR002149; LRI.

CC InterPro; IPR003315; RPH3A\_effector.

CC InterPro; IPR001565; Synaptotagmin.

CC InterPro; IPR00306; Znf\_FYVE.

CC Pfam; PF00168; C2; 2.

CC Pfam; PF03318; RPH3A\_effector; 1.

CC PRINTS; PR00360; C2DOMAIN.

CC PRINTS; PR00399; SYNAPTOTAGMN.

CC SMART; SM00239; C2; 2.

CC PROSITE; PS00499; C2\_DOMAIN\_1; 2.

CC PROSITE; PS50004; C2\_DOMAIN\_2; 2.

CC PROSITE; PS50916; RABBD; 1.

CC PROSITE; PS50178; ZF\_FYVE; 1.

CC Repeat; Synapse; Protein transport; Zinc-finger; 3D-structure.

CC KW Repeat; Synapse; Protein transport; Zinc-finger; 3D-structure.

CC FT DOMAIN 40 157 RAB-BINDING.

CC FT ZN FING 88 145 FIVE-TYPE.

CC FT DOMAIN 280 364 PRO-RICH.

CC FT DOMAIN 384 488 C2 DOMAIN 1.

CC FT DOMAIN 542 645 C2 DOMAIN 2.

CC FT HELIX 50 84

CC FT TURN 85 85

CC FT STRAND 93 93

CC FT TURN 103 100

CC FT STRAND 103 104

CC FT TURN 108 110

CC FT STRAND 112 114

CC FT TURN 117 119

CC FT STRAND 120 121

CC FT TURN 123 125

CC FT STRAND 135 137

CC FT STRAND 138 149

CC FT TURN 150 150

CC FT HELIX 152 155

CC FT TURN 156 156

CC SQ SEQUENCE 684 AA; 75832 MW; 05838BC3C7A86444 CRC64;

Query Match 57.8%; Score 37; DB 1; Length 684;

Best Local Similarity 75.0%; Pred. No. 1.1e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DDLTKLWL 10

DB 577 DPEVKLWL 584

RESULT 30

RP3A\_HUMAN STANDARD; PRT; 694 AA.

AC Q912J0; Q96AB0; 16-OCT-2001 (Rel. 40; Created)

DT 16-OCT-2001 (Rel. 40; Last sequence update)

DT 10-OCT-2003 (Rel. 42; Last annotation update)

DE Rabphilin-3A (Exophilin 1).

GN RPH3A OR KIAA0985.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain.

RX MEDLINE=92246063; PubMed=10231032;

RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirokawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.

RT Prediction of the coding sequences of unidentified human genes. XIII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.

RT DNA Res. 6:63-70(1999).

RL [2]

RN SEQUENCE FROM N.A.

RP TISSUE=Brain.

RC MEDLINE=22388257; PubMed=1247932;

RX Strausberg R.L., Reinhold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci F., Prange C., Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullanb S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E., Jones S.J.M., Matra M.A.

RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -1- FUNCTION: Protein transport. Probably involved with Ras-related protein Rab-3A in synaptic vesicle traffic and/or synaptic vesicle fusion. Could play a role in neurotransmitter release by regulating membrane flow in the nerve terminal (by similarity).

CC -1- SIMILARITY: Contains 2 C2 domains.

CC -1- SIMILARITY: Contains 1 FIVE-type zinc finger.

CC -1- SIMILARITY: Contains 1 Rab-binding (RabBD) domain.

CC -----

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CC -----

CC EMBL; AB023202; BAA76829.1; -

CC EMBL; BC017259; AAI17259.1; -

CC HSSP; P47709; 1ZBD.

CC InterPro; IPR000008; C2.

CC InterPro; IPR008973; C2\_CaLB.

CC InterPro; IPR002149; LRI.

CC InterPro; IPR003315; RPH3A\_effector.

CC InterPro; IPR001565; Synaptotagmin.

CC InterPro; IPR00306; Znf\_FYVE.

CC Pfam; PF00168; C2; 2.

CC Pfam; PF03318; RPH3A\_effector; 1.

CC PRINTS; PR00360; C2DOMAIN.

CC PRINTS; PR00399; SYNAPTOTAGMN.

CC SMART; SM00239; C2; 2.

CC PROSITE; PS00499; C2\_DOMAIN\_1; 2.

CC PROSITE; PS50004; C2\_DOMAIN\_2; 2.

CC PROSITE; PS50916; RABBD; 1.

DR PROSITE; PS50178; ZF FYVE; 1.  
 KW Repeat; Synapse; protein transport; zinc-finger.  
 FT DOMAIN 44 160 RAB-BINDING.  
 FT ZN FING 92 148 FYVE-TYPE.  
 FT DOMAIN 162 375 PRO-RICH.  
 FT DOMAIN 394 498 C2 DOMAIN 1.  
 FT DOMAIN 552 655 C2 DOMAIN 2.  
 FT CONFLICT 24 28 NDKRO -> K (IN REF. 2).  
 SQ SEQUENCE 694 AA; 76872 MW; B99C43F306A04D69 CRC64;  
 Query Match 57.8%; Score 37; DB 1; Length 694;  
 Best Local Similarity 75.0%; Pred. No. 1,1e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 DPLTKML 10  
 DB 587 DPFVKML 594  
 RESULT 31  
 RP3A BOVIN STANDARD; PRT; 704 AA.  
 AC 006846;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Rabphilin-3A (Exophilin 1).  
 GN RPH3A.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
 OC Bovidae; Bovinae; Bos.  
 ON NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=93204952; PubMed=8384302;  
 RA Shirataki H., Kaibuchi K., Sakoda T., Kishida S., Yamaguchi T.,  
 Wada K., Miyazaki M., Takai Y.;  
 RT "Rabphilin-3A, a putative target protein for smg p25A/rab3A p25 small  
 GTP-binding protein related to synaptotagmin.";  
 RT Mol. Cell. Biol. 13:2061-2068(1993).  
 RN [2]  
 RP DOMAINS.  
 RX MEDLINE=94086530; PubMed=8262955;  
 RA Yamaguchi T., Shirataki H., Kishida S., Miyazaki M., Nishikawa J.,  
 Wada K., Numata S.-I., Kaibuchi K., Takai Y.;  
 RT "Two functionally different domains of rabphilin-3A, Rab3A p25/smg  
 p25A-binding and phospholipid- and Ca(2+)-binding domains.";  
 RT J. Biol. Chem. 268:27164-27170(1993).  
 CC -1- FUNCTION: Protein transport. Probably involved with Ras-related  
 vesicle fusion. Could play a role in neurotransmitter release by  
 regulating membrane flow in the nerve terminal.  
 CC -1- SUBUNIT: Monomer.  
 CC -1- TISSUE SPECIFICITY: Specifically expressed in brain.  
 CC -1- SIMILARITY: Contains 2 C2 domains.  
 CC -1- SIMILARITY: Contains 1 FYVE-type zinc finger.  
 CC -1- SIMILARITY: Contains 1 Rab-binding (RabBD) domain.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; D13613; BA002780.1; -;  
 DR PIR; A48097; A48097.  
 DR HSSP; P47709; 1ZBD.  
 DR InterPro; IPR000008; C2.  
 DR InterPro; IPR008973; C2\_CaLB.

DR InterPro; IPR002149; LRI.  
 DR InterPro; IPR003315; RPH3A effector.  
 DR InterPro; IPR001565; Synaptoleptin.  
 DR InterPro; IPR000306; Znf\_FYVE.  
 DR Pfam; PF00168; C2; 2.  
 DR Pfam; PF02318; RPH3A\_effector; 1.  
 DR PRINTS; PR00360; C2DOMAIN.  
 DR PRINTS; PR00399; SYNAPTOTAGMIN.  
 DR SMART; SM00239; C2; 2.  
 DR PROSITE; PS00499; C2 DOMAIN 1; 2.  
 DR PROSITE; PS50004; C2 DOMAIN 2; 2.  
 DR PROSITE; PS50916; RABBD; 1.  
 DR PROSITE; PS50178; ZF FYVE; 1.  
 KW Repeat; Synapse; protein transport; zinc-finger.  
 FT DOMAIN 44 161 RAB-BINDING.  
 FT ZN FING 92 149 FYVE-TYPE.  
 FT DOMAIN 417 508 C2 DOMAIN 1.  
 FT DOMAIN 577 665 C2 DOMAIN 2.  
 SQ SEQUENCE 704 AA; 77977 MW; 132AD048F58F8FD4 CRC64;  
 Query Match 57.8%; Score 37; DB 1; Length 704;  
 Best Local Similarity 75.0%; Pred. No. 1,1e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 DPLTKML 10  
 DB 597 DPFVKML 604  
 RESULT 32  
 MAK2 HUMAN STANDARD; PRT; 819 AA.  
 AC 012851;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Mitogen-activated protein kinase kinase kinase 2 (MEKKK 2)  
 DE (MAPK/ERK kinase kinase 2) (MEK kinase kinase 2) (MEKK 2)  
 DE (germinal center kinase) (GC kinase) (Rab8 interacting protein) (B  
 lymphocyte serine/threonine protein kinase).  
 GN MAP4K2 OR RAB8IP OR GCK.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.  
 RC TISSUE=Testis;  
 RX MEDLINE=94266900; PubMed=7515885;  
 RA Katz P., Whalen G., Kehrl J.H.;  
 RT "Differential expression of a novel protein kinase in human B  
 lymphocytes. Preferential localization in the germinal center.";  
 RT J. Biol. Chem. 269:16802-16809(1994).  
 RN [2]  
 RP FUNCTION, AND INTERACTION WITH TRAF2 AND MAP3K1.  
 RX MEDLINE=2164464; PubMed=11784851.  
 RA Chadee D.N., Yuasa T., Kyriakis J.M.;  
 RT "Direct activation of mitogen-activated protein kinase kinase kinase  
 MEKK1 by the Ste20p homologue GCK and the adapter protein TRAF2.";  
 RT Mol. Cell. Biol. 22:737-748(2002).  
 CC -1- FUNCTION: Enhances MAP3K oligomerization, which may relieve  
 amino-terminal mediated MAP3K autoinhibition and lead to  
 activation following autophosphorylation. May play a role in the  
 regulation of vesicle targeting or fusion.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -1- COFACTOR: Magnesium.  
 CC -1- SUBUNIT: Interacts with TRAF2, MAP3K1 and Rab8/Wel.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Also found as a peripheral  
 membrane protein in the Golgi region and basolateral plasma  
 membrane domains (By similarity).  
 CC -1- TISSUE SPECIFICITY: Highly expressed in germinal center but not  
 mantle zone B-cells. Also expressed in lung, brain and placenta  
 and at lower levels in other tissues examined.

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CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC STRE20 subfamily.
CC -1- SIMILARITY: Contains 1 CNH domain.
CC -----
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CC -----
DR EMBL: U07349; AAA20968.1; -.
DR PIR: A53714; A53714.
DR HSSP: G63450; 1A06.
DR GeneW: HGNC:6864; MAP4K2.
DR MIM: 603166; -.
DR GO: GO:0000139; C:Golgi membrane; TAS.
DR GO: GO:0005625; C:soluble fraction; TAS.
DR GO: GO:0005524; F:ATP binding; IDA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IDA.
DR GO: GO:0007516; P:hemocyte development; TAS.
DR GO: GO:0006955; P:immune response; TAS.
DR GO: GO:0007254; P:JNK cascade; TAS.
DR GO: GO:0006903; P:nonselective vesicle targeting; NAS.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IDA.
DR GO: GO:0006950; P:response to stress; TAS.
DR InterPro: IPR001180; Citron.
DR InterPro: IPR000719; Prot Kinase.
DR InterPro: IPR008271; Ser Thr Pkin AS.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00780; CNH; 1.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SMO0036; CNH; 1.
DR SMART: SMO0220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; FALSE NEG.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 15 272 PROTEIN KINASE.
FT NP BIND 487 799 CNH.
FT BINDING 21 29 ATP (BY SIMILARITY).
FT ACT_SITE 135 135 BY SIMILARITY.
SQ ACT_SITE 819 AA; 91585 MW; 4BD5102005F1653C CRC64;
Query Match 57.8%; Score 37; DB 1; Length 819;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 WYDPTKLMW 10
Db 626 WYEPLOKFL 635

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RESULT 33
M4K2_MOUSE STANDARD; PRT; 821 AA.
ID M4K2_MOUSE
AC Q61161;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitogen-activated protein kinase kinase kinase 2 (EC 2.7.1.37)
DE (MAPK/ERK kinase kinase 2) (MEK kinase kinase 2) (MEKK 2)
DE (Germinal center kinase) (GCK) (Rab8 interacting protein).
GN MAP4K2 OR RAB8IP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, INTERACTION WITH RAB8, AND SUBCELLULAR

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RP LOCATION.
RC STRAIN-BALB/C;
RX MEDLINE=96209873; PubMed=8643544;
RA Ren M., Zeng J., De Lencos-Chiarandini C., Rosenfeld M., Adeunik M.,
RA Sabatini D.D.;
RT "In its active form, the GTP-binding protein rab8 interacts with a
RT stress-activated protein kinase";
RL Proc. Natl. Acad. Sci. U.S.A. 93:5151-5155(1996).
RN [2]
RP SEQUENCE OF 42-821 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=22354683; PubMed=1246851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nishida I., Osato N., Saito R., Suzuki H., Yamataka I., Kiyosawa H.,
RA Yaegaki K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gajobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsumoto H., Batilov S., Beisel K.W.,
RA Blake J.A., Brad D., Brusic V., Choehia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Guetlich S., Hirokawa N., Jackson I.U., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lemhard B., Lyons P.A.,
RA Magdoli D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G.,
RA Petrovsky N., Pillai R., Pontius U.V., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Walstedt C., Wang Y., Warshawsky Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yangisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Zimin P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazawa N., Sato K.,
RA Shiraki T., Waki K., Kawai K., Aizawa K., Arikawa T., Fukuda S.,
RA Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shigaawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
CC -1- FUNCTION: Enhances MAPK1 oligomerization, which may relieve
CC amino-terminal mediated MAPK1 autoinhibition and lead to the
CC activation following autophosphorylation. May play a role in the
CC regulation of vesicle targeting or fusion.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBUNIT: Interacts with TRAF2, MAPK1 and Rab8/Mel.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Also found as a peripheral
CC membrane protein in the Golgi region and basolateral plasma
CC membrane domains.
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC STRE20 subfamily.
CC -1- SIMILARITY: Contains 1 CNH domain.
CC -----
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CC -----
DR EMBL: U50595; AAC52571.1; -.
DR HSSP: AK051036; BAC34507.1; -.
DR HSSP: G63450; 1A06.
DR MGD: MGI:1346883; Map4K2.
DR GO: GO:0005524; F:ATP binding; ISS.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; ISS.
DR GO: GO:0006903; P:nonselective vesicle targeting; IDA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; ISS.
DR GO: GO:0007243; P:protein kinase cascade; ISS.
DR InterPro: IPR001180; Citron.

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DPOL_HSV11 STANDARD; PRT: 985 AA.
AC P28859;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase (EC 2.7.7.7).
GN 57.
OS Ictalurid herpesvirus 1 (Channel catfish virus) (CCV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Ictalurid herpes-like viruses.
OX NCBI_TaxID=10401;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Aburn 1;
RX MEDLINE=92087490; PubMed=1727613;
RA Davison A.J.;
RT "Channel catfish virus: a new type of herpesvirus.";
RL Virology 186:9-14(1992).
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
+ {DNA}(n).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the DNA polymerase type-B family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M75136; AA88160.1; -.
DR PIR; D36792; DUBET1.
DR InterPro; IPR006172; DNA_pol_B.
DR InterPro; IPR006134; DNA_pol_B_dom.
DR Pfam; PF00136; DNA_pol_B_1.
DR PRINTS; PR00106; DNAPOLB.
DR SMART; SM00486; POLBc.1.
DR PROSITE; PS00116; DNA_POLYMERASE_B_1.
DR TRANSFERASE; DNA-directed DNA polymerase; DNA replication;
DR DNA-binding; Nuclear protein.
DR KW
DR SEQUENCE 985 AA; 113468 MW; B15C48927D73385A CRC64;
SQ
Query Match 57.8%; Score 37; DB 1; Length 985;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 2; Gaps 1;
Oy 1 WY--DPLTKLWL 10
|: |||:|:|
Db 893 WVVVDPLTGIMW 904

```

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RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Saito N., Samped G., Seki Y., Sivasubram S., Tagami H.,
RA Takeda J., Takemoto K., Mada C., Yamamoto Y., Horuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [3]
RP SEQUENCE OF 965-1105 FROM N.A.
RX MEDLINE=85054800; PubMed=6094528;
RA Nakabeppu Y., Miyata T., Kondo H., Iwanaga S., Sekiguchi M.;
RT "Structure and expression of the alpha gene of Escherichia coli
RT involved in adaptive response to alkylating agents.";
RL J. Biol. Chem. 259:13730-13736(1984).
RN [4]
RP IDENTIFICATION.
RX MEDLINE=95075659; PubMed=7984428;
RA Borodovsky M., Rudd K.E., Koonin E.V.;
RT "Intrinsic and extrinsic approaches for detecting genes in a
RT bacterial genome.";
RL Nucleic Acids Res. 22:4756-4767(1994).
CC -1- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC -1- SIMILARITY: Contains 3 PAS-associated C-terminal (PAC) domains.
CC -1- SIMILARITY: Contains 1 EAL domain.
CC -1- SIMILARITY: Contains 1 GDEF domain.
CC -----
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CC -----
DR EMBL; AE000296; AAC75128.1; -.
DR EMBL; D90844; BAI15920.1; -.
DR EMBL; D90845; BAI15925.1; -.
DR EMBL; K02498; -; NOT_ANNOTATED_CDS.
DR PIR; B64973; B64973.
DR EcGene; EG12396; Yege.
DR InterPro; IPR001633; EAL.
DR InterPro; IPR000160; GDEF.
DR InterPro; IPR007895; NASEI.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000700; PAS-assoc_C.
DR InterPro; IPR000014; PAS_domain.
DR Pfam; PF00563; EAL.1.
DR Pfam; PF00990; GDEF.1.
DR Pfam; PF05231; NASEI.1.
DR Pfam; PF00785; PAC.3.
DR Pfam; PF00989; PAS.2.
DR SMART; SM00267; DUF1.1.
DR SMART; SM00052; DUF2.1.
DR SMART; SM00086; PAC.3.
DR SMART; SM00086; PAC.3.
DR TIGRFAMs; TIGR00254; GDEF.1.
DR TIGRFAMs; TIGR00229; sensory_box.3.
DR PROSITE; PS50883; EAL.1.
DR PROSITE; PS50887; GDEF.1.
DR PROSITE; PS50113; PAC.3.
DR PROSITE; PS50112; PAS.2.
DR Hypothetical protein; Repeat; Complete proteome.
FT DOMAIN 300 370.
FT DOMAIN 374 426.
FT PAC 1.

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FT DOMAIN 501 552 PAC 2.  
FT DOMAIN 553 623 PAC 2.  
FT DOMAIN 626 680 PAC 3.  
FT DOMAIN 712 845 GDEF.  
FT DOMAIN 855 1104 EAL.  
FT CONFLICT 965 966 EQ -> NS (IN REF. 3).  
SQ SEQUENCE 1105 AA; 123886 MW; 22BE64B963CB9739 CRC64;  
Query Match 57.8%; Score 37; DB 1; Length 1105;  
Best Local Similarity 58.3%; Pred. No. 1.8e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;  
QY 1 WYDPLTKL--WL 10  
Db 114 WYNPLONLADWL 125  
RESULT 37  
ID DEXT STRDO STANDARD; PRT; 1337 AA.  
AC P39653;  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Dextranase precursor (EC 3.2.1.11) (Alpha-1,6-glucan-6-glucanohydrolase).  
GN DEX.  
OS Streptococcus downei (Streptococcus sobrinus).  
OG Plasmid pYA902.  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_Taxid=13117;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-36.  
RX STRAIN=6715 / UAB66;  
RA MEDLINE=94292401; PubMed=8021165;  
RA Wanda S.-Y., Curtiss R. III;  
RT "Purification and characterization of Streptococcus sobrinus dextranase produced in recombinant Escherichia coli and sequence analysis of the dextranase gene.";  
RL J. Bacteriol. 176:3839-3850(1994).  
CC -1- FUNCTION: MAY PLAY A ROLE IN SUCROSE-INDEPENDENT ADHERENCE TO THE PELTICE-COATED TOOTH SURFACE.  
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,6-alpha-D-glucosidic linkages in dextran.  
CC -1- SUBUNIT: Homodimer.  
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (Potential).  
CC -1- MISCELLANEOUS: The activity of this enzyme is optimal at pH 5.3 and at 39 degrees Celsius.  
CC -1- SIMILARITY: Belongs to family 66 of glycosyl hydrolases.  
CC -1- CAUTION: It is uncertain whether Met-1 or Met-5 is the initiator.  
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CC -----  
DR EMBL; M96978; AAA21772.1; -  
DR InterPro; IPR001899; Gram\_pos\_anchor.  
DR Pfam; PF00746; Gram\_pos\_anchor; 1.  
DR TIGRfams; TIGR01167; LPXTG\_anchor; 1.  
DR PROSITE; PS50847; GRAM\_POS\_ANCHORING; 1.  
KW Hydrolyase; Glycosidase; Cell wall; Peptidoglycan-anchor; Repeat;  
KW Signal; Plasmid.  
FT SIGNAL 1 30  
FT CHAIN 1 1308  
FT PROPEP 1309 1337  
FT SITE 1305 1309  
MOD\_RSS 1308 1308  
DEXTANASE.  
REMOVED BY SORTAGE (POTENTIAL).  
LPXTG SORTING SIGNAL (POTENTIAL).  
AMIDE-LINKED TO CELL WALL (POTENTIAL).

SQ SEQUENCE 1337 AA; 143298 MW; B494275A77A2E3D0 CRC64;  
Query Match 57.8%; Score 37; DB 1; Length 1337;  
Best Local Similarity 55.6%; Pred. No. 2.2e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 1 WYDPLTKLW 9  
Db 423 YINPTSKLW 431  
RESULT 38  
ID METH MYCSE STANDARD; PRT; 1206 AA.  
AC Q49775; Q9C37; Q9S378;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE 5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13) (Methionine synthase, vitamin-B12 dependent isozyme) (MS).  
GN METH OR MLI307 OR MLCB2533.04 OR B2126\_C1\_157.  
OS Mycobacterium lepreae.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_Taxid=1769;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Smith D.R., Robison K.;  
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TN;  
RX MEDLINE=21128732; PubMed=11234002;  
RA Cole S.T., Englemer K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Humphrey S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Rutter S., Seeger K., Simm S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrett B.G.;  
RT "Massive gene decay in the leprosy bacillus.";  
RL Nature 409:1007-1011(2001).  
CC -1- CATALYTIC ACTIVITY: 5-methyltetrahydrofolate + L-homocysteine = tetrahydrofolate + L-methionine.  
CC -1- COFACTOR: Cobaltamin (By similarity).  
CC -1- PATHWAY: Terminal step in the de novo biosynthesis of methionine.  
CC -1- SIMILARITY: Belongs to the vitamin-B12 dependent methionine synthase family.  
CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 873.  
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CC -----  
DR EMBL; U00017; AAA17182.1; ALT FRAM.  
DR EMBL; AL035310; CAA22918.1; ALT INIT.  
DR EMBL; AL583921; CAC31686.1; -  
DR PIR; B87072; B87072.  
DR HSSP; P13009; 1BMT.  
DR Leproma; MLI307; -  
DR InterPro; IPR006158; B12-binding.  
DR InterPro; IPR003759; CoMet synth B12.  
DR InterPro; IPR000489; Dhdropt synth.  
DR InterPro; IPR004223; Met synth B12.  
DR InterPro; IPR003726; S\_methyl\_Trans.  
Pfam; PF02310; B12-binding; 1.

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DR Pfam: PF02607; B12-binding 2; 1.
DR Pfam: PF02965; Met synt B12; 1.
DR Pfam: PF00809; Pectin_bind; 1.
DR Pfam: PF02574; S-methyl_trans; 1.
DR Transferrase; Methyltransferase; Methionine biosynthesis; Vitamin B12;
KW Cobalt; Complete proteome.
FT DOMAIN 751 830 COBALAMIN-BINDING (POTENTIAL).
FT METRL 753 753 COBALAMIN-BINDING (POTENTIAL).
SQ SEQUENCE 1206 AA; 133392 MW; 7786CE5307D7CA86 CRC64;

Query Match 57.0%; Score 36.5; DB 1; Length 1206;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 2 YDPLTKL-WL 10
DB 620 YDPLQKLMWL 629

RESULT 39
ID Y302_MYCGE STANDARD; PRT; 317 AA.
AC P47544;
CD 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG302.
GN MG302.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA Tomb J.-F., Dougherty B.A., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RL "The minimal gene complement of Mycoplasma genitalium.";
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U39710; AAC71524.1; -.
DR PIR: D64233; D64233.
DR TIGR: MG302; -.
DR InterPro: IPR003339; CblQ.
DR Pfam: PF02361; CblQ; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 18 38 POTENTIAL.
FT TRANSMEM 58 78 POTENTIAL.
FT TRANSMEM 92 112 POTENTIAL.
FT TRANSMEM 130 150 POTENTIAL.
FT TRANSMEM 159 179 POTENTIAL.
FT TRANSMEM 202 222 POTENTIAL.
FT TRANSMEM 252 272 POTENTIAL.
SQ SEQUENCE 317 AA; 36667 MW; BCG9741BD5283680 CRC64;

Query Match 56.2%; Score 36; DB 1; Length 317;
Best Local Similarity 85.7%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 DPLTKLM 9

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DB 11 DPLTKLM 17

RESULT 40
ID POSL_HUMAN STANDARD; PRT; 359 AA.
AC O06416; Q9BZV9;
CD 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE POU domain, class 5, transcription factor 1-like protein 1 (Occamer
DE binding protein 3-like).
GN POU5F1P1 OR POU5F1C8 OR OTF3C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93027160; PubMed=1408763;
RA Takeda J., Seino S., Bell G.I.;
RT "Human Oct3 gene family: cDNA sequences, alternative splicing, gene
RT organization, chromosomal location, and expression at low levels in
RT adult tissues.";
RL Nucleic Acids Res. 20:4613-4620 (1992).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA van Roozendaal K.E.P., Gillis A.J.M., van Asseldonk M.,
RA Oosterhuis J.W., Looijenga L.H.J., van Zoelen B.J.J.;
RT "Identification and expression analysis of novel intron-less human
RT POU5F1/OCT3 related POU domain genes.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Belongs to the POU transcription factor family.
CC Class-5 subfamily.
CC -1- SIMILARITY: Contains 1 homeobox domain.
CC -1- SIMILARITY: Contains 1 homeobox domain.
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CC -----
DR EMBL: Z11901; CAAT7953.1; -.
DR EMBL: AF268615; AAG53083.1; -.
DR TRANSFAC: T04471; -.
DR Genew: HGNC:9223; POU5F1P1.
DR HSSP: P20263; 10CP.
DR GO: GO:0005634; C:nucleus; TAS.
DR GO: GO:0003700; F:transcription factor activity; TAS.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
DR InterPro: IPR001356; Homeobox.
DR InterPro: IPR007103; POU domain.
DR Pfam: PF00046; homeobox; 1.
DR Pfam: PF00157; pou; 1.
DR PRINTS: PR00028; POUDOMAIN.
DR ProDom: PD000010; Homeobox; 1.
DR ProDom: PD000583; POU domain; 1.
DR SMART: SM00389; HOX; 1.
DR SMART: SM00352; POU; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS00071; HOMEBOX_2; 1.
DR PROSITE: PS00035; POU_1; 1.
DR PROSITE: PS00465; POU_2; FALSE NEG.
KW DNA-binding; Homeobox; Nuclear protein.
FT DOMAIN 138 212 POU.
FT DNA_BIND 229 288 HOMEBOX.

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FT CONFLICT 197 197 I -> M (IN REF. 2).  
SQ SEQUENCE 359 AA; 38570 MW; 9FBD440CEC4DD9A CRC64;

Query Match 56.2%; Score 36; DB 1; Length 359;  
Best Local Similarity 70.0%; Pred. No. 83;  
Matches 7; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 WYDPLTKLWL 10  
| | | | |  
DB 29 WVDPLT--WL 36

## RESULT 41

POS5\_HUMAN STANDARD; PRT; 359 AA.  
AC Q9BZV7;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DE POU domain, class 5, transcription factor 1-like protein 2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OX Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
RN NCBI\_TaxID=9606;  
[1]

## SEQUENCE FROM N.A.

RA van Roozendaal K.E.P., Gillis A.J.M., van Asseldonk M.,  
Oosterhuis J.W., Looijenga L.H.J., van Zoelen E.J.J.,  
RT "Identification and expression analysis of novel intron-less human  
RT POU5F1/OCT3 related POU domain genes";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
CC -1- SIMILARITY: Belongs to the POU transcription factor family.  
CC -1- SIMILARITY: Contains 1 homeobox domain.  
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DR EMBL: AF266618; AAC53085.1; -.  
DR HSPF; P20253; 10CP.  
DR InterPro; IPR001356; Homeobox.  
DR InterPro; IPR000327; POU domain.  
DR InterPro; IPR007103; POU\_homeo.  
DR Pfam; PF00046; homeobox; 1.  
DR Pfam; PF00157; pou; 1.  
DR PRINTS; PR00028; POU\_DOMAIN.  
DR ProDom; PD000010; Homeobox; 1.  
DR ProDom; PD000583; POU\_domain; 1.  
DR SMART; SM00389; HOX; 1.  
DR SMART; SM00352; POU; 1.  
DR PROSITE; PS00027; HOMEBOX\_1; 1.  
DR PROSITE; PS00071; HOMEBOX\_2; 1.  
DR PROSITE; PS00035; POU\_1; 1.  
DR PROSITE; PS00465; POU\_2; 1.  
DR DNA-binding; Homeobox; Nuclear protein.  
FT DOMAIN 138 212 POU.  
FT DNA\_BIND 229 288 HOMEBOX.  
SQ SEQUENCE 359 AA; 38562 MW; C5D9513CE3E1690 CRC64;

Query Match 56.2%; Score 36; DB 1; Length 359;  
Best Local Similarity 70.0%; Pred. No. 83;  
Matches 7; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 WYDPLTKLWL 10  
| | | | |  
DB 29 WVDPLT--WL 36

## RESULT 42

GAL7\_TRIE STANDARD; PRT; 382 AA.  
AC Q96011;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DE Galactose-1-phosphate uridylyltransferase (EC 2.7.7.12) (gal-1-P  
DE uridylyltransferase) (UDP-glucose--hexose-1-phosphate  
DE uridylyltransferase).  
GN GAL7.  
OS Trichoderma reesei (Hypocrea jecorina).  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Hypocreomycetidae; Hypocerales; Hypocreaceae; Hypocrea.  
OX NCBI\_TaxID=51453;  
RN [1]

## SEQUENCE FROM N.A.

RC STRAIN=QM9414 / Rut C-30;  
RA Seiboth B., Hofmann G., Kubicek C.P.;  
RT "Lactose metabolism and cellulase production in *Hypocrea jecorina*: the  
RT gal7 (galactose-1-phosphate uridylyltransferase) gene is essential for  
RT growth on galactose but not for cellulase induction";  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: UDP-glucose + alpha-D-galactose 1-phosphate =  
CC alpha-D-glucose 1-phosphate + UDP-galactose.  
CC -1- COFACTOR: Binds 1 zinc and 1 iron ion per subunit (Potential).  
CC -1- PATHWAY: Galactose metabolism; second step.  
CC -1- SIMILARITY: Belongs to the galactose-1-phosphate  
CC uridylyltransferase family 1.  
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DR EMBL: AY057108; AAL14201.1; -.  
DR InterPro; IPR001937; Galp\_UDPtransf1.  
DR InterPro; IPR005851; Galp\_Utransf1.  
DR InterPro; IPR005851; Galp\_Utransf1.  
DR InterPro; IPR005849; Galp\_Utransf1.  
DR Pfam; PF02744; Galp\_UDP\_tr\_C; 1.  
DR Pfam; PF01087; Galp\_UDP\_tr\_C; 1.  
DR ProDom; PD005051; Galp\_UDPtransf1.  
DR TIGRPFAMs; TIGR00209; galT 1; 1.  
DR PROSITE; PS00117; GAL\_P\_UDP\_TRANSF\_1; 1.  
DR TRANSFERASE; Nucleotidyltransferase; Galactose metabolism; zinc; iron;  
KM Metal-binding.  
FT ACT\_SITE 198 198 NUCLEOPHILE (BY SIMILARITY).  
FT METAL 55 55 ZINC (POTENTIAL).  
FT METAL 196 196 ZINC (POTENTIAL).  
FT METAL 214 214 IRON (POTENTIAL).  
FT METAL 313 313 IRON (POTENTIAL).  
FT METAL 330 330 IRON (POTENTIAL).  
FT METAL 332 332 IRON (POTENTIAL).  
SQ SEQUENCE 382 AA; 43780 MW; 25A08CC695C39794 CRC64;

Query Match 56.2%; Score 36; DB 1; Length 382;  
Best Local Similarity 66.7%; Pred. No. 89;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLWL 10  
| : | | | |  
DB 14 YNPLTDSWL 22

RESULT 43  
O42B\_DROME STANDARD; PRT; 399 AA.  
ID \_O42B\_DROME



AC 09V914;  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Putative odorant receptor 42b.  
 GN OR42B OR CG12754.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydriidae; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RC MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amaratunga P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton R.C., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chape M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.W., Basu A., Baxendale J., Bayraktaroglu L., Beaskey E.M.,  
 RA Beeson K.Y., Bencos P.V., Bertman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos J.M., Delcher S., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hoselin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mates B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Modarres C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,  
 RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Sideri-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
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 RP REVISIONS.  
 RX MEDLINE=22426069; PubMed=12537572;  
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 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
 CC -1- FUNCTION: Probable role in the odorant response, being an odorant  
 CC receptor.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).  
 CC -1- SIMILARITY: Belongs to family Dr-or of G-protein coupled  
 CC receptors.  
 CC -----  
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DR EMBL, AE003785; AAF57305.2; -  
 DR Flybase; FBgn003043; Or42b.  
 DR GO; GO:0016021; C:integral to membrane; NAS.  
 DR GO; GO:0004984; F:olfactory receptor activity; NAS.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; NAS.  
 DR GO; GO:0007608; P:olfaction; NAS.  
 DR InterPro; IPR004117; 7tm\_6.  
 DR Pfam; PF02949; 7tm\_6; 1.  
 KW Hypothetical protein; Transmembrane; G-protein coupled receptor;  
 KW Glycoprotein; Olfaction; Multigene family.  
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CC 1 WYDPLTKLML 10  
DB 222 WHDPVKCRWL 231

RESULT 46  
ARIL\_HUMAN STANDARD; PRT; 503 AA.  
ID ARIL\_HUMAN STANDARD; PRT; 503 AA.  
AC Q94981; 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Ariadne-1 protein (Ari-1).  
GN ARI-1 OR ARI OR CG5659.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
NCBI\_TaxID=7227;

CC [1]  
CC SEQUENCE FROM N.A., CHARACTERIZATION, AND MUTAGENESIS.  
CC STRAIN=Oregon-R;  
CC MEDLINE=20341325; PubMed=10880484;  
CC Aguilar M., Olivares M., Martinez-Padron M., Barbas J.A., Ferrus A.;  
CC "Ariadne-1: a vital Drosophila gene is required in development and  
CC defines a new conserved family of ring-finger proteins.";  
CC Genetics 155:1231-1244(2000).  
CC [2]  
CC SEQUENCE FROM N.A.  
CC STRAIN=Berkley;  
CC MEDLINE=20196006; PubMed=10731132;  
CC Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
CC Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
CC George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
CC Sutcliffe G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
CC Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chame M., Pfeiffer B.D.,  
CC Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
CC Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
CC Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
CC Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
CC Botkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,  
CC Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
CC Chertey J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
CC de Pablos B., Delcher A., Deng Z., Deslattes Mays A., Dew I.,  
CC Dietz S.M., Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S.,  
CC Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C.,  
CC Ferreira S., Fleischmann W., Foster C., Gabrielson A.E., Gary N.S.,  
CC Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z.,  
CC Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J.,  
CC Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J.,  
CC Wel M.-H., Idegawa C., Jalali M., Kalish F., Karpen G.H., Ke Z.,  
CC Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C.,  
CC Kravitz S., Kulp D., Lai Z., Lasok P., Lei Y., Levitsky A.A., Li J.,  
CC Li Z., Liang Y., Lin X., Liu X., Matrei B., McIntosh T.C.,  
CC McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C.,  
CC Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L.,  
CC Musker D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K.,  
CC Nusskern D.R., Paclob J.M., Palazolo M., Peltman G.S., Pan S.,  
CC Pollard J.D., Puri V., Reese M.G., Reinert K., Remington K.,  
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CC Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C.,  
CC Stjepic M., Strong R., Sun E., Svitskas R., Tector D., Turner R.,  
CC Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A.,  
CC Weinsbach G.M., Weisenbach J., Williams S.M., Woodage T.,  
CC Wolley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S.,  
CC Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N.,  
CC Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W.,  
CC Rubin G.M., Venter J.C.;  
CC "The genome sequence of Drosophila melanogaster";  
CC Science 287:2185-2195(2000).  
CC -1- FUNCTION: Might act as an E3 ubiquitin-protein ligase, or as part  
CC of E3 complex, which accepts ubiquitin from specific E2 ubiquitin-

CC conjugating enzymes, such as UBCHD10/UBR2L3, and then transfers it  
CC to substrates.  
CC -1- SUBUNIT: Interacts with UBCHD10. Can form dimers.  
CC -1- SUBCELLULAR LOCATION: Mainly cytoplasmic.  
CC -1- TISSUE SPECIFICITY: Widely expressed, with prominent levels in the  
CC nervous system and female gonads.  
CC -1- DEVELOPMENTAL STAGE: Expressed in all tissues throughout  
CC development, with maximum levels reached during metamorphosis and  
CC maintained in the adult.  
CC -1- SIMILARITY: Contains 2 RING-type zinc fingers.  
CC -1- SIMILARITY: Contains 1 IBR-type zinc finger.  
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CC EMBL: X98309; CA66953.1; -;  
CC DR EMBL: X98310; CA66954.1; -;  
CC DR EMBL: AB003507; AAF4807.1; -;  
CC DR FLYBASE: FBgn0017418; ari-1.  
CC DR InterPro: IPR002867; Znf\_C6HC.  
CC DR InterPro: IPR001841; Znf\_fing.  
CC DR Pfam: PF01485; IBR; 1.  
CC DR SMART: SM00647; IBR; 2.  
CC DR SMART: SM00184; RING; 2.  
CC DR PROSITE: PS00518; ZF\_RING\_1; FALSE\_NEG.  
CC DR PROSITE: PS50089; ZF\_RING\_2; 1.  
CC DR UniProt: P50089; ZF\_RING\_2; 1.  
CC KM Ub1 conjugation pathway; Zinc-finger, Repeat; Coiled coil.  
CC FT DOMAIN 22 27 ASP-RICH (ACIDIC).  
CC FT ZN\_FING 133 182 RING-TYPE 1.  
CC FT ZN\_FING 203 264 IBR-TYPE.  
CC FT ZN\_FING 291 336 RING-TYPE 2.  
CC FT DOMAIN 133 201 INTERACTION WITH UBCHD10.  
CC FT DOMAIN 341 361 COILED COIL (POTENTIAL).  
CC FT MUTAGEN 150 150 C->Y: IN ARI1-2; LETHAL PHENOTYPE AND  
CC LOSS OF INTERACTION WITH UBCHD10.  
CC FT C->Y: IN ARI1-3; LETHAL PHENOTYPE AND NO  
CC LOSS OF INTERACTION WITH UBCHD10.  
CC FT MUTAGEN 309 309  
CC SQ SEQUENCE 503 AA; 58932 MW; 0AECCB256CF5EC00 CRC64;

Query March 56.2%; Score 36; DB 1; Length 503;  
Best Local Similarity 50.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

CC 1 WYDPLTKLML 10  
DB 258 WHDPVKCRWL 267

RESULT 47  
ARIL\_HUMAN STANDARD; PRT; 557 AA.  
ID ARIL\_HUMAN STANDARD; PRT; 557 AA.  
AC Q974X5; Q76026; Q9H376; Q9UENO; Q9UP39;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ariadne-1 protein homolog (Ari-1) (ubiquitin-conjugating enzyme E2-  
DE binding protein 1) (Ubch7-binding protein) (Ubchm-interacting protein)  
DE (HHR1) (H7-AP2) (HUS5-27) (MOP-6).  
GN ARI1 OR ARI OR UBCH7BP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
NCBI\_TaxID=9606;  
CC [1]  
CC SEQUENCE FROM N.A.  
CC TISSUE=Fetal brain;  
CC MEDLINE=99452997; PubMed=10521492;  
CC Moynihan T.P., Ardley H.C., Nuber U., Rose S.A., Jones P.F.,

RA Markham A.F., Scheffner M., Robinson P.A.;  
 RT "The ubiquitin-conjugating enzymes UbcH7 and UbcH8 interact with RING  
 RT finger/IBR motif-containing domains of HHARI and H7-AP1.";  
 RL J. Biol. Chem. 274:30963-30968(1999).  
 RN [2]  
 RP REVISIONS TO 227.  
 RA Ardley H.C.;  
 RL Unpublished observations (MAY-2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Trockenbacher A., Marksteiner R., Schneider R.;  
 RT "Human ariadne homolog.";  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heich F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stempelson M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rana S.S., Lochellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bostak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gills R.A.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Pahey J., Holtom E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butcherfield Y.S.N., Krzywicki M.I., Skalska U., Smallos D.E.,  
 RA Scheraga A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [5]  
 RP SEQUENCE OF 95-557 FROM N.A.  
 RA MEDLINE=20341325; PubMed=10880484;  
 RA Aguilera M., Oliveros M., Martinez-Padron M., Barbas J.A., Ferrus A.;  
 RT "Aridine-1: a vital Drosophila gene is required in development and  
 RT defines a new conserved family of ring-finger proteins.";  
 RL Genetics 155:1231-1244(2000).  
 RN [6]  
 RP SEQUENCE OF 298-557 FROM N.A.  
 RC TISSUE=Brain;  
 RA MEDLINE=21064499; PubMed=11124703;  
 RA Stanchi F., Bertocco E., Toppi S., Dioguardi R., Simonati B.,  
 RA Cannata N., Zimbello R., Lanfranchi G., Valle G.;  
 RT "Characterization of 16 novel human genes showing high similarity to  
 RT yeast sequences.";  
 RL Yeast 18:65-80(2001).  
 RN [7]  
 RP SEQUENCE OF 377-557 FROM N.A.  
 RC TISSUE=Monocytes;  
 RA Fujii Y., Takayama K., Ukai Y., Yoshimoto M.;  
 RT "Molecular and biological characterization of a new ring finger  
 RT protein, MOP-6 which is highly expressed in activated human  
 RT monocytes.";  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RP INTERACTION WITH UBE2L3, AND MUTAGENESIS OF GUN-187, ILE-188, CYS-  
 RP 208 AND TYR-258.  
 RX MEDLINE=21276469; PubMed=11278816;  
 RA Ardley H.C., Tan N.G.S., Rose S.A., Markham A.F., Robinson P.A.;  
 RT "Features of the parkin/ariadne-like ubiquitin ligase, HHARI, that  
 RT regulate its interaction with the ubiquitin-conjugating enzyme,  
 RT UbcH7.";  
 RL J. Biol. Chem. 276:19640-19647(2001).  
 CC -1- FUNCTION: Might act as an E3 ubiquitin-protein ligase, or as part  
 CC of the E3 complex, which accepts ubiquitin from specific E2

CC ubiquitin-conjugating enzymes, such as UBE2L3/UBC4, and then  
 CC transfers it to substrates.  
 CC -1- SUBUNIT: Interacts with UBE2L3.  
 CC -1- SUBCELLULAR LOCATION: Mainly cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: Widely expressed.  
 CC -1- SIMILARITY: Contains 2 RING-type zinc fingers.  
 CC -1- SIMILARITY: Contains 1 IBR-type zinc finger.  
 CC -----  
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 DR EMBL; AJ243190; CAB45870.1; ALT\_SEQ.  
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 DR EMBL; AJ009771; CAA08817.1; -.  
 DR EMBL; AB014774; BAB19786.1; -.  
 DR Genbank; HGNC:689; ARIH1.  
 DR MIM; 605624; -.  
 DR GO; GO:0000151; C:ubiquitin ligase complex; TAS.  
 DR GO; GO:0019899; F:enzyme binding; IPI.  
 DR GO; GO:0019787; F:ubiquitin-like-protein ligase activity; TAS.  
 DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; TAS.  
 DR Interpro; IPR002867; Znf\_C6HC.  
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GN KHLH8 OR KIAA1378.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
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 RC TISSUE=Brain;  
 RA MEDLINE=20181126; PubMed=10718198;  
 RA Nagase T., Kikuno R., Ishikawa K.-I., Hirose M., Ohara O.,  
 RT "Prediction of the coding sequences of unidentified human genes. XVI.  
 RT The complete sequences of 150 new cDNA clones from brain which code  
 RT for large proteins in vitro."  
 RL DNA Res. 7:65-73(2000).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Klausner R.D., Collins P.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheeler C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshynski S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Pahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,  
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- SIMILARITY: Contains 1 BTF/POZ domain.  
 CC -1- SIMILARITY: Contains 6 Kelch repeats.  
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 CC -----  
 DR EMBL; AB037799; BAA92616.2; ALT\_INIT.  
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 DR Genew; HGNC:18644; KHLH8.  
 DR InterPro; IPR000210; BTF\_POZ.  
 DR InterPro; IPR006651; Kelch.  
 DR InterPro; IPR006652; Kelch\_rep.  
 DR Pfam; PF00651; BTF; 1.  
 DR Pfam; PF01344; Kelch; 6.  
 DR PRINTS; PR00501; KELCHREPEAT.  
 DR SMART; SM00225; BTF; 1.  
 DR SMART; SM00612; Kelch; 6.  
 DR PROSITE; PSS0097; BTF; 1.  
 KW Kelch repeat; Repeat.  
 FT DOMAIN 67 134 BTF.  
 FT REPEAT 319 366 KELCH 1.  
 FT REPEAT 367 413 KELCH 2.  
 FT REPEAT 415 460 KELCH 3.  
 FT REPEAT 462 507 KELCH 4.  
 FT REPEAT 508 554 KELCH 5.  
 FT REPEAT 556 601 KELCH 6.  
 FT CONFLICT 520 520 R -> P (IN REF. 1).  
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Best Local Similarity 55.6%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 OY 2 YDPLTKML 10  
 DB 386 FDLTKML 394  
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 KHLH8 MOUSE STANDARD; PRT; 629 AA.  
 ID ID P59280;  
 AC 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Kelch-like protein 8.  
 GN KHLH8.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
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 RX MEDLINE=22354683; PubMed=12466851;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nishikido I., Osato N., Saito R., Suzuki H., Yamakita I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schmidt L.M., Knapman A., Matsuda H.A., Batalov S., Beisel K.W.,  
 RA Blake J.A., Brad D., Brusic V., Chochia C., Corbani L.E., Cousins S.,  
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 RA Grimmond S., Gustinchik S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
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 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
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 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sadelain A., Schneider C., Semple C.A., Setou M., Shimada K.,  
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 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Warshawsky Y., Wells C.,  
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 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Takahara T., Kono H., Nakamura M., Sakezune N., Sato K.,  
 RA Shitaki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.,  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 CC -1- SIMILARITY: Contains 1 BTF/POZ domain.  
 CC -1- SIMILARITY: Contains 6 Kelch repeats.  
 CC -----  
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 DR EMBL; AK049960; BAC34008.1; --  
 DR MGD; MGI:2179430; Khlh8.  
 DR InterPro; IPR000210; BTF\_POZ.  
 DR InterPro; IPR006651; Kelch.  
 DR InterPro; IPR006652; Kelch\_rep.  
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 DR Pfam; PF01344; Kelch; 6.  
 DR PRINTS; PR00501; KELCHREPEAT.

Query Match 56.2%; Score 36; DB 1; Length 620;

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DR SMART; SM00612; Kelch; 6.
DR PROSITE; PS00097; BTB; 1.
KW Kelch repeat; Repeat.
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FT REPEAT 76 143 BTB.
FT REPEAT 328 375 KELCH 1.
FT REPEAT 376 422 KELCH 2.
FT REPEAT 424 469 KELCH 3.
FT REPEAT 471 516 KELCH 4.
FT REPEAT 517 563 KELCH 5.
FT REPEAT 565 610 KELCH 6.
SQ SEQUENCE 629 AA; 69816 MW; 684F04801A94934B CRC64;

Query Match 56.2%; Score 36; DB 1; Length 629;
Best Local Similarity 55.6%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKML 10
DB 395 FDLTKMKM 403

RESULT 50
CSLA PEDHE
ID _CSLA_PEDHE STANDARD; PRT; 700 AA.
AC Q59286;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Chondroitinase AC precursor (EC 4.2.2.5) (Chondroitin AC lyase)
DE (Chondroitin sulfate AC lyase) (Chondroitin AC eliminase).
GN CSLA OR CHNAC.
OS Pedobacter heparinum (Flavobacterium heparinum).
OC Bacteri; Bacteroidetes; Sphingobacteriales;
OC Sphingobacteriaceae; Pedobacter.
OX NCBI_TaxID=984;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13125;
RX MEDLINE=20087513; PubMed=10618199;
RA Tkalet A.L., Fluk D., Blain F., Zhang-Sun G., Laliberte M.,
RA Bennett D.C., Gu K., Zimmermann J.J.F., Su H.;
RT "Isolation and expression in Escherichia coli of csLA and csLB, genes
RT coding for the chondroitin sulfate-degrading enzymes chondroitinase
RT AC and chondroitinase B, respectively, from Flavobacterium
RT heparinum.",
RT Appl. Environ. Microbiol. 66:29-35 (2000).
[2]
RN RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=99264394; PubMed=10329169;
RA Fethiere J., Eggimann B., Cygler M.;
RT "Crystal structure of chondroitin AC lyase, a representative of a
RT family of glycosaminoglycan degrading enzymes.",
RT J. Mol. Biol. 288:635-647 (1999).
[3]
RN RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=2126222; PubMed=11327856;
RA Huang W., Boju L., Tkalet A.L., Su H., Yang H.O., Gunay N.S.,
RA Linhardt R.J., Kim Y.S., Matte A., Cygler M.;
RT "Active site of chondroitin AC lyase revealed by the structure of
RT enzyme-oligosaccharide complexes and mutagenesis.",
RT Biochemistry 40:2359-2372 (2001).
CC -1- CATALYTIC ACTIVITY: Elimination degradation of polysaccharides
CC containing 1,4-beta-D-hexosaminy and 1,3-beta-D-glucuronosyl
CC linkages to disaccharides containing 4-deoxy-beta-D-gluc-4-
CC enuronosyl groups.
CC -1- COFACTOR: Binds 1 calcium ion per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- SIMILARITY: Belongs to the polysaccharide lyase family 8.
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DR EMBL; U27583; AAC8383.1; -.
DR PDB; 1CB8; 14-MAY-99.
DR PDB; 1HM2; 02-MAY-01.
DR PDB; 1HM3; 02-MAY-01.
DR PDB; 1HMU; 02-MAY-01.
DR PDB; 1HMV; 02-MAY-01.
DR InterPro; IPR008929; Chondroitin_lyas.
DR InterPro; IPR003159; Lyase_8.
DR InterPro; IPR004103; Lyase_8_C.
DR Pfam; PF02278; Lyase_8; 1.
DR Pfam; PF02884; Lyase_8_C; 1.
KW Lyase; Signal; Glycoprotein; Calcium; 3D-structure.
FT SIGNAL 1 22
FT CHAIN 23 700 CHONDROITINASE AC.
FT ACT_SITE 225 225
FT ACT_SITE 234 234
FT ACT_SITE 288 288
FT METAL 405 405 CALCIUM.
FT METAL 407 407 CALCIUM.
FT METAL 416 416 CALCIUM.
FT METAL 417 417 CALCIUM (VIA CARBONYL OXYGEN).
FT CARBOHYD 328 328 O-LINKED (MAN. . .).
FT CARBOHYD 455 455 O-LINKED (MAN. . .).
SQ SEQUENCE 700 AA; 79693 MW; C36B608FCAPFC656 CRC64;

Query Match 56.2%; Score 36; DB 1; Length 700;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PLTKLW 9
DB 422 PLTKLW 427

RESULT 51
MAKS_HUMAN
ID _MAKS_HUMAN STANDARD; PRT; 846 AA.
AC Q9Y4K4; Q81YF6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mitogen-activated protein kinase kinase kinase 5 (EC 2.7.1.37)
DE (MAPK/ERK kinase kinase 5) (MEK kinase kinase 5) (MEKKK 5)
DE (kinase homologous to SPK1/STR20) (KHS).
GN MAPK5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932;
RA Strusberg R.L., Feinold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shmelen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diachenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carinici P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RL [3]  
 RP INTERACTION WITH CRK AND CRKL.  
 RX MEDLINE=99002481; PubMed=9788432;  
 RA Oenli W., Kardinal C., Ruf S., Adermann K., Groffen J., Feng G.-S.,  
 RA Blenis J., Tan T.-H., Feller S.M.;  
 RT "The germinal center kinase (GCK)-related protein kinases HPR1 and KHS  
 RT are candidates for highly selective signal transducers of Ctk family  
 RT adapter proteins.";  
 CC Oncogene 17:1893-1901 (1998).  
 CC -1- FUNCTION: May play a role in the response to environmental stress.  
 CC -1- Appears to act upstream of the c-jun N-terminal pathway.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -1- SUBUNIT: Interacts with both SH3 domains of the adapter proteins  
 CC CRK and CRKL.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: Ubiquitously expressed in all tissues  
 CC examined with high levels in the ovary, testis and prostate.  
 CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
 CC ST120 subfamily.  
 CC -1- SIMILARITY: Contains 1 CNH domain.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

FT DOMAIN 512 826 CNH.  
 FT MUTAGEN 49 49 K->R: LOSS OF KINASE ACTIVITY AND ABILITY  
 FT. CONFLICT 473 473 N->K (IN REF. 2).  
 SQ SEQUENCE 846 AA; 95039 MW; B17F95196AA14E08 CRC64;  
 Query Match 56.2%; Score 36; DB 1; Length 846;  
 Best Local Similarity 50.0%; Pred. No. 2e+02; Indels 0; Gaps 0;  
 Matches 5; Conservative 2; Mismatches 3;  
 Qy 1 WYDPLTKML 10  
 Db 651 WYEPMKFML 660  
 RESULT 52  
 MAK5 MOUSE STANDARD; PRT; 847 AA.  
 ID 08BPM2; O8CJ05; O8CGF3; O9JLM7; Q9CX73;  
 AC 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Mitogen-activated protein kinase kinase kinase 5 (EC 2.7.1.37)  
 DE (MAPK/ERK kinase kinase 5) (MEK kinase kinase 5) (MEKKK 5).  
 GN MAPK5.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 OX [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC STRAIN=C57BL/6J; TISSUE=Fetal eye, Fetal liver, and Fetal lung;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Aikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 RA Aikawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fletschmann W., Gaasterland T., Gissi C., King B., Kochia H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schiraldi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Funo M., Aono H., Baldarelli R., Baren G.,  
 RA Blake J., Boffelli D., Bojunga N., Carinici P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Guertlich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momtazs P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata K., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsaki S.,  
 RA Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690 (2001).  
 RP [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC STRAIN=Czech II; TISSUE=Mammary gland;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helt F.,  
 RA Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant J.L., Scheetz T.B.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carinici P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,



RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: May play a role in the response to environmental stress.  
 CC Appears to act upstream of the c-jun N-terminal pathway (By  
 CC similarity).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -1- COFACTOR: Magnesium (By similarity).  
 CC -1- SUBUNIT: Interacts with both SH3 domains of the adapter proteins  
 CC CRK and CRKL (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=QBPM2-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=QBPM2-2; Sequence=VSP\_050478;  
 CC Note=NO experimental confirmation available;  
 CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
 CC STE20 subfamily.  
 CC -1- SIMILARITY: Contains 1 CNH domain.  
 CC -----  
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 CC -----  
 DR EMBL: AK019468; BAB31739.1; -  
 DR EMBL: AK053775; BAC35517.1; -  
 DR EMBL: AK048891; BAC39305.1; -  
 DR EMBL: BC040381; AAH40381.1; ALT\_INIT.  
 DR EMBL: BC002309; AAH02309.1; -  
 DR HSSP: P24941; 1B38.  
 DR MGD: MGI:1925503; Map4k5.  
 DR GO: GO:0005737; C:cytoplasm; ISS.  
 DR GO: GO:0005524; F:ATP binding; ISS.  
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; ISS.  
 DR GO: GO:0006468; P:protein amino acid phosphorylation; ISS.  
 DR GO: GO:0007243; P:protein kinase cascade; ISS.  
 DR GO: GO:0006950; P:response to stress; ISS.  
 DR InterPro: IPR001180; Citron.  
 DR InterPro: IPR0082719; Prot\_kinase.  
 DR InterPro: IPR008271; Ser\_Thr\_kinase.  
 DR InterPro: IPR002290; Ser\_Thr\_kinase.  
 DR InterPro: IPR001245; Tyr\_kinase.  
 DR Pfam: PF00780; CNH; 1.  
 DR Pfam: PF00069; pkinase; 1.  
 DR ProDom: PD000001; Prot\_kinase; 1.  
 DR SMART: SM00036; CNH; 1.  
 DR SMART: SM00220; S\_TKc; 1.  
 DR SMART: SM00219; TyrKc; 1.  
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.  
 DR PROSITE: PS00108; PROTEIN KINASE ST; FALSE NEG.  
 DR ATP-binding; Transferase; Serine/threonine-protein kinase;  
 KW Alternative splicing;  
 KW DOMAIN  
 FT NP\_BIND 20 277  
 FT BINDING 26 34  
 FT ACT\_SITE 49 49  
 FT ACT\_SITE 140 140  
 FT DOMAIN 501 827  
 FT VARSP 294 312  
 FT VARSP 312 312  
 FT CONFLICT 79 79  
 FT CONFLICT 103 103  
 FT CONFLICT 118 118  
 FT CONFLICT 441 441  
 FT CONFLICT 727 727  
 FT SEQUENCE 847 AA; 95044 MW; 3770E9FC6ECPA3 CRC64;

Query Match 56.2%; Score 36; DB 1; Length 847;  
 Best local similarity 50.0%; Pred. No. 2e+02;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 WYDPLTKMLT 10  
 DB 652 WYEPWQKEML 661  
 RESULT 53  
 DEXT\_STRMU  
 ID DEXT\_STRMU STANDARD; PRT; 850 AA.  
 AC Q54443;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Dextranase precursor (EC 3.2.1.11) (Alpha-1,6-glucan-6-  
 DE glucanohydrolase).  
 GN DEXA OR SMU.2042.  
 OS Streptococcus mutans.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1309;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Ingbritt;  
 RX MEDLINE=96245544; PubMed=8657012;  
 RA Igasaki T., Yamamoto A., Goto N.;  
 RT "Sequence analysis of the Streptococcus mutans Ingbritt dexa gene  
 RT encoding extracellular dextranase.";  
 RL Microbiol. Immunol. 39:853-860(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Ingbritt;  
 RX MEDLINE=96081507; PubMed=8535521;  
 RA Colby S.M., Whiting G.C., Tao L., Russell R.R.B.;  
 RT "Insertional inactivation of the Streptococcus mutans dexa  
 RT (dextranase) gene results in altered adherence and dextran  
 RT catabolism.";  
 RL Microbiology 141:2929-2936(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=UA159 / ATCC 700610 / Serotype C;  
 RX MEDLINE=22295063; PubMed=12397186;  
 RA Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,  
 RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,  
 RA Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;  
 RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental  
 RT pathogen.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).  
 CC -1- FUNCTION: MAY PLAY A ROLE IN SUCROSE-INDEPENDENT ADHERENCE TO THE  
 CC PELICLE-COATED TOOTH SURFACE.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,6-alpha-D-glucosidic  
 CC linkages in dextran.  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by  
 CC an amide bond (potential).  
 CC -1- SIMILARITY: Belongs to family 66 of glycosyl hydrolases.  
 CC -----  
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 CC -----  
 DR EMBL: D49430; BA08409.1; -  
 DR EMBL: AE015026; AAN59642.1; -  
 DR InterPro: IPR001899; Gram\_pos\_anchor.  
 DR Pfam: PF00746; Gram\_pos\_anchor; 1.  
 DR TIGRfam: TIGR01167; LPXtg\_anchor; 1.



DR PROSITE: PS50847; GRAM\_POS ANCHORING; 1.  
 KW Hydrolase; Glycosidase; Cell wall; Peptidoglycan-anchor; Signal;  
 KW Complete proteome.  
 FT SIGNAL 1 ? 814 DEXTRANSASE.  
 FT CHAIN 815 850 REMOVED BY SORTASE (POTENTIAL).  
 FT PROPEP 811 815 LPTG SORTING SIGNAL (POTENTIAL).  
 FT SITE 814 814 AMIDE-LINKED TO CELL WALL (POTENTIAL).  
 FT MOD\_RES 16 16 A -> N (IN REF. 1 AND 2).  
 FT CONFLICT 22 22 T -> A (IN REF. 1 AND 2).  
 FT CONFLICT 39 39 V -> A (IN REF. 1 AND 2).  
 FT CONFLICT 56 56 G -> E (IN REF. 1 AND 2).  
 FT CONFLICT 67 67 S -> P (IN REF. 1 AND 2).  
 FT CONFLICT 141 141 A -> V (IN REF. 1 AND 2).  
 FT CONFLICT 376 376 N -> T (IN REF. 1 AND 2).  
 FT CONFLICT 504 504 V -> I (IN REF. 1 AND 2).  
 FT CONFLICT 704 704 A -> T (IN REF. 1 AND 2).  
 FT CONFLICT 707 707 I -> V (IN REF. 1 AND 2).  
 FT CONFLICT 776 776 VDE -> BDG (IN REF. 1 AND 2).  
 FT CONFLICT 783 783 I -> L (IN REF. 1 AND 2).  
 FT CONFLICT 849 849 K -> N (IN REF. 1 AND 2).  
 SQ SEQUENCE 850 AA; 94482 MW; FCF3E7DF7B4EA178 CRC64;  
 Query Match 56.2%; Score 36; DB 1; Length 850;  
 Best Local Similarity 55.6%; Pred. No. 2e+02;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 WYDPLTKLM 9  
 DB 354 YYNPLSKSM 362  
 RESULT 54  
 ID POL\_IPHA STANDARD; PRT; 863 AA.  
 AC P04026;  
 DT 23-OCT-1986 (Rel. 02, Last sequence update)  
 DT 23-OCT-1986 (Rel. 02, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Putative POL polypeptide [contains: Endonuclease; Reverse  
 DE transcriptase (EC 2.7.7.49)].  
 GN POL.  
 OS Hamster intracisternal A-particle (IAP-H18).  
 OC Viruses; Retroviral viruses; Retroviridae; Intracisternal A-particles.  
 OK NCBI\_TaxID=11752;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85264989; PubMed=2991563;  
 RA Ono M., Toh H., Miyata T., Awaya T.;  
 RT "Nucleotide sequence of the Syrian hamster intracisternal A-particle  
 RT gene: close evolutionary relationship of type A particle gene to  
 RT types B and D oncovirus genes.";  
 RL J. Virol. 55:387-394(1985).  
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate  
 CC + [DNA] (N).  
 CC -1- MISCELLANEOUS: READTHROUGH OF THREE TERMINATORS MAY OCCUR: TAA  
 CC BETWEEN CODONS ATT FOR 660-ILE AND AAA FOR 661-LYS, TAG BETWEEN  
 CC CODONS TCC FOR 832-SER AND TAT FOR 833-TYR, AND TAG BETWEEN CODONS  
 CC CCC FOR 859-PRO AND ATT FOR 860-ILE.  
 DR PIR: A03964; GNMHYH.  
 DR HSSP: P03355; IIML.  
 DR InterPro: IPR001037; Integrase\_C.  
 DR InterPro: IPR003308; Integrase\_Zn.  
 DR InterPro: IPR002156; RNaseH.  
 DR InterPro: IPR001584; Rve.  
 DR InterPro: IPR000477; RYase.  
 DR Pfam: PF00552; Integrase\_1.  
 DR Pfam: PF02022; Integrase\_Zn\_1.  
 DR Pfam: PF00075; RNaseH\_1.  
 DR Pfam: PF00665; rve; 1.  
 DR Pfam: PF00078; rvc; 1.  
 KW Transferase; RNA-directed DNA polymerase; Hydrolase; Nuclease;  
 KW Endonuclease; Polypeptide.

SQ SEQUENCE 863 AA; 97036 MW; 704AE7FC6B1D86 CRC64;  
 Query Match 56.2%; Score 36; DB 1; Length 863;  
 Best Local Similarity 56.7%; Pred. No. 2e+02;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 OY 1 WYDPLTKLM 9  
 DB 764 WKDVLTDLM 772  
 RESULT 55  
 ID JMJ2\_HUMAN STANDARD; PRT; 1064 AA.  
 AC O75164;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE JmJ2 domain containing protein 2.  
 GN JMJ2 OR KIAA0677.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OK NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=98403880; PubMed=9734811;  
 RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,  
 RA Kotani H., Nomura N., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. X.  
 RT The complete sequences of 100 new cDNA clones from brain which can  
 RT code for large proteins in vitro.";  
 RL Nucleic Acids Res. 5:169-176(1998).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg K.H., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stjepicon M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
 RA Brownstein M.J., Umed T.B., Toshimaki S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- SIMILARITY: Contains 1 JMJ2 domain.  
 CC -1- SIMILARITY: Contains 1 JMJN domain.  
 CC -1- SIMILARITY: Contains 2 Tudor domains.  
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 DR EMBL: AB014577; BAA31652.1;  
 DR EMBL: BC002558; AA02558.1;  
 DR Genbank: U000000; JMJ2.



10-OCT-2003 (Rel. 42, Last annotation update)  
DE C-Jun-amino-terminal kinase interacting protein 3 (JNK-interacting  
DE protein 3) (JIP-3) (JNK MAP kinase scaffold protein 3) (Mitogen-  
DE activated protein kinase 8-interacting protein 3) (JNK-Associated  
DE protein 1) (JSAPI) (Sunday driver 2).  
GN MAPK8IP3 OR JSAPI OR JIP3 OR SYD2.  
OC Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OC NCBI\_taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1A), FUNCTION, PHOSPHORYLATION, AND  
RP INTERACTION WITH MAPK8, MAPK9, MAPK10, MAPK14 AND MAPK1.  
RC TISSUE=Brain;  
RX MEDLINE=99455010; PubMed=10523642;  
RA Ito M., Yoshida K., Akechi M., Yamashita S., Takamatsu N.,  
RA Sugiyama K., Hibi M., Nakabeppu Y., Shiba T., Yamamoto K.-I.,  
RA "JSAPI, a novel Jun N-terminal protein kinase (JNK)-binding protein  
RT that functions as a scaffold factor in the JNK signaling pathway.";  
RL Mol. Cell. Biol. 19:7539-7548(1999).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1A, 1B, 1C, 1D AND 1E), AND TISSUE  
RP SPECIFICITY.  
RC TISSUE=Brain;  
RX MEDLINE=20480689; PubMed=11024282;  
RA Ito M., Akechi M., Hirose R., Ichimura M., Takamatsu N., Xu P.,  
RA Nakabeppu Y., Tadaoishi S., Yamamoto K.-I., Yoshida K.,  
RT "Isoforms of JSAPI scaffold protein generated from alternative  
RT splicing.";  
RL Gene 255:229-234(2000).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS 1C AND 3A), FUNCTION, INDUCTION, TISSUE  
RP SPECIFICITY, SUBCELLULAR LOCATION, PHOSPHORYLATION, MUTAGENESIS OF  
RP ARG-205, PRO-206; THR-207; SER-208; LEU-209; THR-266; THR-276 AND  
RP THR-287, AND INTERACTION WITH MAPK8IP2; MAPK9; MAPK10; MAPK17  
RP AND MAPK11.  
RC STRAIN=C57BL/6; TISSUE=Brain, and Heart;  
RX MEDLINE=20094982; PubMed=1062960;  
RA Kelkar N., Gupta S., Dickens M., Davis R.J.,  
RT "Interaction of a mitogen-activated protein kinase signaling module  
RT with the neuronal protein JIP3.";  
RL Mol. Cell. Biol. 20:1030-1043(2000).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 1C), SUBCELLULAR LOCATION, AND INTERACTION  
RP WITH KLC1.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RX MEDLINE=20560743; PubMed=11106729;  
RA Bowman A.B., Kamal A., Ritchings B.W., Philp A.V., McGrail M.,  
RA Gidhart J.G., Goldstein L.S.B.,  
RT "Kinesin-dependent axonal transport is mediated by the Sunday Driver  
RT (SYD) protein.";  
RL Cell 103:583-594(2000).  
RN [5]  
RP SEQUENCE OF 1240-1337 FROM N.A.  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hilyk S.W.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stjepanovic M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carrincci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmitt J., Myers R.W.,  
RA Buterfield V.S.N., Krzywinski M.I., Skalski N., Smallus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [6]  
RP INTERACTION WITH KLC.  
RC TISSUE=Brain;  
RX MEDLINE=21135887; PubMed=11238452;  
RA Verhey K.J., Meyer D., Deehan R., Blenis J., Schnapp B.J.,  
RA Rapoport T.A., Margolis B.,  
RT "Cargo of kinesin identified as JIP scaffolding proteins and  
RT associated signaling molecules.";  
RL J. Cell Biol. 152:959-970(2001).  
RN [7]  
RP SEQUENCE FROM N.A. (ISOFORM 1A), FUNCTION, PHOSPHORYLATION, AND  
RP INTERACTION WITH MAPK8, MAPK9, MAPK10, MAPK14 AND MAPK1.  
RC TISSUE=Brain;  
RX MEDLINE=20480689; PubMed=11024282;  
RA Ito M., Yoshida K., Akechi M., Yamashita S., Takamatsu N.,  
RA Sugiyama K., Hibi M., Nakabeppu Y., Shiba T., Yamamoto K.-I.,  
RA "JSAPI, a novel Jun N-terminal protein kinase (JNK)-binding protein  
RT that functions as a scaffold factor in the JNK signaling pathway.";  
RL Mol. Cell. Biol. 19:7539-7548(1999).  
RN [8]  
RP SEQUENCE FROM N.A. (ISOFORMS 1A, 1B, 1C, 1D AND 1E), AND TISSUE  
RP SPECIFICITY.  
RC TISSUE=Brain;  
RX MEDLINE=20480689; PubMed=11024282;  
RA Ito M., Akechi M., Hirose R., Ichimura M., Takamatsu N., Xu P.,  
RA Nakabeppu Y., Tadaoishi S., Yamamoto K.-I., Yoshida K.,  
RT "Isoforms of JSAPI scaffold protein generated from alternative  
RT splicing.";  
RL Gene 255:229-234(2000).  
RN [9]  
RP SEQUENCE FROM N.A. (ISOFORMS 1C AND 3A), FUNCTION, INDUCTION, TISSUE  
RP SPECIFICITY, SUBCELLULAR LOCATION, PHOSPHORYLATION, MUTAGENESIS OF  
RP ARG-205, PRO-206; THR-207; SER-208; LEU-209; THR-266; THR-276 AND  
RP THR-287, AND INTERACTION WITH MAPK8IP2; MAPK9; MAPK10; MAPK17  
RP AND MAPK11.  
RC STRAIN=C57BL/6; TISSUE=Brain, and Heart;  
RX MEDLINE=20094982; PubMed=1062960;  
RA Kelkar N., Gupta S., Dickens M., Davis R.J.,  
RT "Interaction of a mitogen-activated protein kinase signaling module  
RT with the neuronal protein JIP3.";  
RL Mol. Cell. Biol. 20:1030-1043(2000).  
RN [10]  
RP SEQUENCE FROM N.A. (ISOFORM 1C), SUBCELLULAR LOCATION, AND INTERACTION  
RP WITH KLC1.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RX MEDLINE=20560743; PubMed=11106729;  
RA Bowman A.B., Kamal A., Ritchings B.W., Philp A.V., McGrail M.,  
RA Gidhart J.G., Goldstein L.S.B.,  
RT "Kinesin-dependent axonal transport is mediated by the Sunday Driver  
RT (SYD) protein.";  
RL Cell 103:583-594(2000).  
RN [11]  
RP SEQUENCE OF 1240-1337 FROM N.A.  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hilyk S.W.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stjepanovic M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carrincci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmitt J., Myers R.W.,  
RA Buterfield V.S.N., Krzywinski M.I., Skalski N., Smallus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length



DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein MJ1570.  
 GN MJ1570.  
 OS Methanococcus jannaschii.  
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;  
 CC Methanocaldococcaceae; Methanocaldococcus.  
 NCBI\_TaxID=2190;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;  
 RX MEDLINE=96337999; PubMed=8688087;  
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,  
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,  
 RA Kere J., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,  
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,  
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,  
 RA Utermbeck T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,  
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,  
 RA Klenk H.-P., Fraser C.M., Smith H.O., Moese C.R., Venter J.C.;  
 RA "Complete genome sequence of the methanogenic archaeon, Methanococcus  
 RT jannaschii.";  
 RL Science 273:1058-1073(1996).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- SIMILARITY: TO M.THERMOAUTOTROPHICUM MTH1706.  
 CC -----  
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 CC -----  
 CC EMBL; U67597; AAB9594.1; -  
 DR TIGR; MJ1570; -  
 DR PIR; A64496; A64496.  
 KW Hypothetical protein; Transmembrane; Complete proteome.  
 FT TRANSMEM 11 31 POTENTIAL.  
 FT TRANSMEM 85 105  
 SO SEQUENCE 115 AA; 12632 MW; 7DEA63DE6131C6A8 CRC64;  
 Query Match 54.7%; Score 35; DB 1; Length 115;  
 Best Local Similarity 60.0%; Pred. No. 38;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 WYDPLTKML 10  
 Db 3 WQDPLVKKFL 12  
 RESULT 60  
 ID RNHL\_HUMAN STANDARD; PRT; 299 AA.  
 AC 075792; 096F11;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ribonuclease HI large subunit (EC 3.1.26.-) (RNase HI large subunit)  
 DE (RNase H(35)) (Ribonuclease H2) (RNase H2).  
 GN RNASBH2A OR RNASBHI OR RNH1A.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=99007233; PubMed=9789007;  
 RA Frank P., Braunhofer-Reiter C., Wintereberger U., Grimm R.,  
 RA Buesen W.;  
 RT "Cloning of the cDNA encoding the large subunit of human RNase HI, a  
 RT homologue of the prokaryotic RNase HI.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:12872-12877(1998).

RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22386257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Umedin T.B., Toshimiyuki S., Carninci P., Prange C.,  
 RA Bata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Rana S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Foley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Wyere R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,  
 RA Scherch A., Schein J.B., Jones S.J.W., Maizra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: Degrades the ribonucleotide moiety on RNA-DNA hybrid  
 CC molecules. Participates in DNA replication.  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-  
 CC phosphomonoester.  
 CC -1- SIMILARITY: Belongs to the RNase H1 family. Eukaryotic subfamily.  
 CC -----  
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 CC -----  
 CC EMBL; Z97029; CAB09725.1; -  
 DR EMBL; BC011748; AAH11748.1; -  
 DR HSSP; Q57599; 1EKE.  
 DR Genew; HGNC:18518; RNASBH2A.  
 DR MIM; 606034; -  
 DR GO; GO:0004540; P:ribonuclease activity; TAS.  
 DR GO; GO:0006260; P:DNA replication; TAS.  
 DR GO; GO:0006401; P:RNA catabolism; TAS.  
 DR InterPro; IPR001352; RNase\_H1/H11.  
 DR InterPro; IPR004649; Rnh11-  
 DR Pfam; PF01351; RNase\_H1; 1.  
 DR TIGRFAMs; TIGR00729; TIGR00729; 1.  
 KW Hydroxylase; Nuclease; Endonuclease.  
 FT ACT\_SITE 34 34  
 FT ACT\_SITE 141 141 BY SIMILARITY.  
 FT ACT\_SITE 169 169 BY SIMILARITY.  
 FT CONFLICT 152 152 R->O (in Ref. 1).  
 SO SEQUENCE 299 AA; 33395 MW; 34992F8B5130157B CRC64;  
 Query Match 54.7%; Score 35; DB 1; Length 299;  
 Best Local Similarity 75.0%; Pred. No. 1e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 DPLTKML 10  
 Db 213 DPKTKML 220  
 RESULT 61  
 ID RNHL\_MOUSE STANDARD; PRT; 301 AA.  
 AC 09CWY8;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)

```

DE Ribonuclease HI large subunit (EC 3.1.26.-) (RNase HI large subunit).
GN RNASEH2A OR RNASEH2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryonic stem cells;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glass C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nakado T., Pesole G., Quackenbush J.,
RA Schiml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaerts P.,
RA Norioka P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- FUNCTION: Degrades the ribonucleotide moiety on RNA-DNA hybrid
CC molecules. Participates in DNA replication (By similarity).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
CC phosphomonester.
CC -1- SIMILARITY: Belongs to the RNase HII family. Eukaryotic subfamily.
CC
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CC
CC EMBL: AK010292; BAB2628.1; -.
CC HSSP: OS7599; 1EXE.
DR MGD: MG1:1916974; 240006P09R1.
DR InterPro: IPR001352; RNase_HII/HIII.
DR InterPro: IPR004649; RnH1.
DR Pfam: PF01351; RNase_HII.1.
DR TIGRPFAM: TIGR00729; TIGR00729.1.
KW Hydrolyase; Nuclease; Endonuclease.
FT ACT SITE 34 34 BY SIMILARITY.
FT ACT SITE 142 142 BY SIMILARITY.
FT ACT SITE 170 170 BY SIMILARITY.
SQ SEQUENCE 301 AA; 33541 MW; ADF92D23F1DB43BF CRC64;

Query Match 54.7%; Score 35; DB 1; Length 301;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DPLTKML 10
DB 214 DPKTKML 221

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RESULT 62
PNN2_ANASP STANDARD; PRT; 306 AA.
AC Q82074;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

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DE Probable inorganic polyphosphate/ATP-NAD kinase 2 (EC 2.7.1.23)
GN (Poly(P)/ATP NAD kinase 2).
OS PNN2 OR AUR0227.
OX Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
[1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21595285; PubMed=11759840;
RX Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriyuchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsunoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimp S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.,
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
CC -1- FUNCTION: Catalyzes the phosphorylation of NAD to NADP. Utilizes
CC ATP and other nucleoside triphosphates as well as inorganic
CC polyphosphate as a source of phosphorus (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + NAD(+) = ADP + NADP(+).
CC -1- COFACTOR: Divalent metal ions (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the NAD kinase family.
CC
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CC
CC EMBL: AP003581; BAB7751.1; -.
DR PIR: A1835; A1835.
DR HAMAP: MF_00361; -1.
DR InterPro: IPR002504; ATP_NADK.
DR Pfam: PF01513; NAD_Kinase_1.
KW "transferase; Kinase; NAD; NADP; Complete proteome.
SQ SEQUENCE 306 AA; 33933 MW; 92FF532CF3D15A6 CRC64;

Query Match 54.7%; Score 35; DB 1; Length 306;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKML 10
DB 241 YDLSTKMLM 249

RESULT 63
YPOR_ACICA STANDARD; PRT; 315 AA.
AC P07783;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in PQO-III 3' region (ORF R) (Fragment).
OS Acinetobacter calcoaceticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=471;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=LMD 79.41;
RX MEDLINE=89123056; PubMed=2536663;
RA Goosen N., Horsman H.P.A., Huinen R.G.M., van de Putte P.,
RT "Acinetobacter calcoaceticus genes involved in biosynthesis of the
RT coenzyme pyridoxal-5-phosphate: nucleotide sequence and
RT expression in Escherichia coli K-12.";
RL J. Bacteriol. 171:447-455(1989).
CC -1- FUNCTION: Not known.
CC -1- SIMILARITY: TO AN ORF IN THE 5' REGION OF PQOA IN K. PNEUMONIAE.

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QY	2	YDPLTKLWL	10
			:
Db	4	YDPFRKKWI	12

— — — — —

Db 316 WYSPLTE 322

SECRET

ER24\_SCHPO  
ID\_FB34 SCHPO  
STAYN

16-OCT-2001 (Sat) 40

DT	28-FEB-2003	(Rel. 41
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DE (Sterol C14-reductas

**Schizosaccharomyces**

Schizosaccharomyceta

NCBI\_TaxID=4896;



[1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SP66;  
 RX MEDLINE=95212923; PubMed=7698661;  
 RA Smith S.;  
 RT "Cloning and sequence analysis of an ERG24 homolog from  
 RT Schizosaccharomyces pombe";  
 RL Gene 155:139-140(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=21848401; PubMed=11859360;  
 RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,  
 RA Gentile S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holtroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagsle K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., Mclean J.,  
 RA Moorey P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Smeuninx M., Squares R., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volckaert G., Aert R., Robben J., Gymnopoulos B.,  
 RA Welford I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Leinrich R., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Leleau V., Motter S.,  
 RA Galbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurt S.M.,  
 RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garçon A., Rhode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez L., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Pothakkin J.,  
 RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;  
 RT "The genome sequence of Schizosaccharomyces pombe";  
 RL Nature 415:871-880(2002).  
 CC -1- FUNCTION: REDUCES THE C14=C15 DOUBLE BOND OF 4,4-DIMETHYL-  
 CC CHOLESTA-8,14,24-TRIENOL TO PRODUCE 4,4-DIMETHYL-CHOLESTA-8,24-  
 CC DIENOL (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: 4,4-dimethyl-5-alpha-cholesta-8,24-dien-3-  
 CC beta-ol + NADP(+) = 4,4-dimethyl-5-alpha-cholesta-8,14,24-trien-3-  
 CC beta-ol + NADPH.  
 CC -1- PATHWAY: Ergosterol biosynthesis.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).  
 CC -1- SIMILARITY: Belongs to the ERG4/ERG24 family.  
 CC -----  
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 CC -----  
 CC EMBL, L36039; AA74121.1; -;  
 CC EMBL, AL023554; CA19037.1; -;  
 CC PIR, JC4057; JC4057.  
 CC DR GeneDB Spombe; SPBC16G5.18; -;  
 CC DR InterPro: IPR001171; ERG4 ERG24.  
 CC DR Pfam: PF01222; ERG4\_ERG24\_1.  
 CC DR PROSITE, PS01017; STEROL\_REDUCT\_1; 1.  
 CC DR PROSITE, PS01018; STEROL\_REDUCT\_2; 1.  
 CC KW Sterol biosynthesis; Oxidoreductase; NADP; Transmembrane.  
 CC FT TRANSMEM 19 39  
 CC FT TRANSMEM 112 132 POTENTIAL.  
 CC FT TRANSMEM 370 390 POTENTIAL.  
 CC SQ SEQUENCE 424 AA; 48560 MW; 1DCCE704F1E5F5B CRC64;  
 Query Match 54.7%; Score 35; DB 1; Length 424;  
 Best Local Similarity 55.6%; Pred. No. 1.5e02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKW 9  
 DB 72 WFTLTLLW 80  
 RESULT 69  
 MK08\_XENLA STANDARD; PRT; 426 AA.  
 AC Q8QHK8; Q8JJC3; (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Mitogen-activated protein kinase 8 (EC 2.7.1.37) (Stress-activated  
 DE protein kinase JNK1).  
 GN JNK1.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OK NCBI\_TaxID=8395;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, COFACTOR, TISSUE  
 RP SPECIFICITY, AND ENZYME REGULATION.  
 RC TISSUE=Oocyte;  
 RX MEDLINE=21657088; PubMed=11751577;  
 RA Yamana H., Moriguchi T., Masuyama N., Kusakabe M., Hanafusa H.,  
 RA Takada R., Takada S., Nishida E.;  
 RT "JNK functions in the non-canonical Wnt pathway to regulate convergent  
 RT extension movements in vertebrates";  
 RL EMBO Rep. 3:69-75(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RA Klein S., Strausberg R.;  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Responds to activation by environmental stress and pro-  
 CC inflammatory cytokines by phosphorylating a number of  
 CC transcription factors, and thus regulating transcriptional  
 CC activity (By similarity). Regulates morphogenic cell movements,  
 CC controlling convergent extension during gastrulation.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -1- COFACTOR: Magnesium.  
 CC -1- ENZYME REGULATION: Activated by threonine and tyrosine  
 CC phosphorylation, potentially by the dual-specificity kinase, MKK7.  
 CC -1- INDIRECTLY ACTIVATED BY: Mnt5a.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=2; Synonym=Beta;  
 CC IsoId=Q8QHK8-1; Sequence=displayed;  
 CC Name=1; Synonym=Alpha;  
 CC IsoId=Q8QHK8-2; Sequence=VSP\_007348, VSP\_007349;  
 CC -1- TISSUE SPECIFICITY: Strongly expressed in presumptive ectoderm and  
 CC mesoderm regions and weakly expressed in endoderm regions during  
 CC dorsal stages of embryo development. Expressed in the head and  
 CC dorsal regions during neurula and tailbud stages.  
 CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. MAP  
 CC kinase subfamily.  
 CC -----  
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 CC -----  
 CC EMBL, AB073999; BAB85483.1; -;  
 CC EMBL, AB074000; BAB81438.1; -;  
 CC EMBL, BC046834; AAH46834.1; -;  
 CC HSSP; P24941; 1BUH.  
 CC GO; GO:0005634; C:nucleus; ISS.  
 CC GO; GO:0004705; F:JUN kinase activity; ISS.

DR GO; GO:0009795; P:embryonic morphogenesis; IDA.  
 DR GO; GO:0007254; P:JNK cascade; ISS.  
 DR InterPro; IPR008351; JNK MAPK.  
 DR InterPro; IPR003527; MAP\_kin.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_kin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR Pfam; PF00069; pkinase.1.  
 DR PRINTS; PR01772; JNKMAPKINASE.  
 DR ProDom; PD000001; Prot\_kinase.1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR SMART; SM00219; Tyrc; 1.  
 DR PROSITE; PS01351; MAPK; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE\_NEG.  
 DR PROSITE; PS00101; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE\_ST; 1.  
 DR ATP-binding; Transferase; Serine/threonine-protein kinase;  
 KW Phosphorylation; Developmental protein; Alternative splicing.  
 FT DOMAIN 26 321 PROTEIN KINASE.  
 FT NP\_BIND 33 38 ATP (BY SIMILARITY).  
 FT BINDING 55 55 BY SIMILARITY.  
 FT ACT\_SITE 151 151 BY SIMILARITY.  
 FT MOD\_RES 183 183 PHOSPHORYLATION (ACTIVATES THE KINASE)  
 FT MOD\_RES 185 185 (BY SIMILARITY).  
 FT MOD\_RES 185 185 PHOSPHORYLATION (ACTIVATES THE KINASE)  
 FT VARSPPLIC 380 384 GAAVT -> AOVQO (in isoform 1).  
 FT VARSPPLIC 385 426 /FTid=VSP\_007348.  
 FT VARSPPLIC 385 426 Missing (in isoform 1).  
 FT VARSPPLIC 385 426 /FTid=VSP\_007348.  
 SQ SEQUENCE 426 AA; 47928 MW; 51990E50A556092 CRC64;

Query Match 54.7%; Score 35; DB 1; Length 426;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPL 5  
 Db 324 WYDPL 328

RESULT 70  
 FTSM MYCLE STANDARD; PRT; 465 AA.  
 AC 050186;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Probable cell division protein ftsm.  
 GN FTSM OR RODA OR ML0019.  
 OS Mycobacterium leprae.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxId=1769;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Fsihi H., Salazar L., Takiff H.E., Cole S.T.;  
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TN;  
 RX MEDLINE=21128732; PubMed=11234002;  
 RA Cole S.T., Elgimeier K., Parkhill J., James K.D., Thomson N.R.,  
 RA Wheeler P.R., Basham D., Garnier T., Churcher C., Harris D.,  
 RA Mungall K., Mungall K., Brown D., Chillingworth T., Connor R.,  
 RA Davies R.M., Devlin K., Duthoy S., Felwell T., Fraser A., Hamlin N.,  
 RA Holroyd S., Hornsby T., Jags K., Lacroix C., Maclean J., Moule S.,  
 RA Rutter S., Oliver K., Quail W.A., Rajandream M.A., Rutherford K.M.,  
 RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,  
 RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,  
 RA Barrell B.G.;  
 "Massive gene decay in the leprosy bacillus."

RL Nature 409:1007-1011 (2001).  
 CC -!- FUNCTION: This is a septum-peptidoglycan biosynthetic protein,  
 CC involved in cell wall formation. Plays a role in the stabilization  
 CC of the free ring during cell division (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -!- SIMILARITY: BELONGS TO THE FTSM/RODA/SPOVE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; Z70722; CA94715.1; -.  
 DR EMBL; AL583917; CAC9527.1; -.  
 DR PIR; G86911; C86911.  
 DR PIR; T10012; T10012.  
 DR Leproma; ML0019; -.  
 DR InterPro; IPR001182; Cell cycle.  
 DR Pfam; PF01098; FTSM RODA SPOVE; 1.  
 DR PROSITE; PS00428; FTSM RODA SPOVE; 1.  
 KW Peptidoglycan synthesis; Cell wall; Cell division; Cell shape;  
 KW Transmembrane; Complete proteome.  
 FT TRANSMEM 22 42 POTENTIAL.  
 FT TRANSMEM 50 70 POTENTIAL.  
 FT TRANSMEM 76 96 POTENTIAL.  
 FT TRANSMEM 115 135 POTENTIAL.  
 FT TRANSMEM 144 164 POTENTIAL.  
 FT TRANSMEM 179 199 POTENTIAL.  
 FT TRANSMEM 222 242 POTENTIAL.  
 FT TRANSMEM 243 263 POTENTIAL.  
 FT TRANSMEM 264 284 POTENTIAL.  
 FT TRANSMEM 308 328 POTENTIAL.  
 FT TRANSMEM 340 360 POTENTIAL.  
 FT TRANSMEM 382 402 POTENTIAL.  
 FT TRANSMEM 414 434 POTENTIAL.  
 FT TRANSMEM 414 434 POTENTIAL.  
 FT CONFLICT 319 320 GI -> VY (IN REF. 1).  
 SQ SEQUENCE 465 AA; 50468 MW; CA656039538EBC24 CRC64;

Query Match 54.7%; Score 35; DB 1; Length 465;  
 Best Local Similarity 62.5%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WYDPLTKL 8  
 Db 294 WMDPFTNL 301

RESULT 71  
 BGAL SULSH STANDARD; PRT; 489 AA.  
 AC P50388;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Beta-galactosidase (EC 3.2.1.23) (Lactase).  
 GN BGLY.  
 OS Sulfolobus shibatae.  
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;  
 OC Sulfolobus.  
 OX NCBI\_TaxId=2286;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 51178 / DSM 5389 / B12;  
 RA Comaritis H., Charalambos B.M.;  
 RA "The development and application of genetical techniques for the  
 RT extremely thermocophilic archaeon Sulfolobus shibatae";  
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-  
 CC galactose residues in beta-D-galactosides.  
 CC -!- SUBUNIT: Homotetramer.

CC -1- SIMILARITY: Belongs to family 1 of glycosyl hydrolases.  
CC -----  
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CC -----  
DR EMBL: L47841; AAA79030.1; -.  
DR HSSP: P22498; 1GOW.  
DR InterPro: IPR001360; Glyco\_hydro\_1.  
DR Pfam: PF00232; Glyco\_hydro\_1; 1.  
DR PRINTS: PR00131; GLHYDRLASE1.  
DR ProDom: PD000650; Glyco\_hydro\_1; 1.  
DR PROSITE: PS00572; GLYCOSYL\_HYDROL\_F1\_1; 1.  
DR PROSITE: PS00653; GLYCOSYL\_HYDROL\_F1\_2; 1.  
KW Hydrolase; Glycosidase.  
FT ACT\_SITE 206 206 PROTON DONOR (POTENTIAL).  
FT ACT\_SITE 387 387 NUCLEOPHILE (BY SIMILARITY).  
SQ SEQUENCE 489 AA; 56564 MW; 32412888f478842b CRC64;  
Query Match 54.7%; Score 35; DB 1; Length 489;  
Best Local Similarity 75.0%; Pred. No. 1.7e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 2 YDELTKLW 9  
Db 369 YDLTKYW 376  
RESULT 72  
BEGAL\_SULSO STANDARD; PRT; 489 AA.  
ID \_BEGAL\_SULSO  
AC P22498; Q9V2Z5;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Beta-galactosidase (EC 3.2.1.23) (Lactase).  
OS LACS OR SSO3019.  
NS Sulfolobus solfataricus.  
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;  
OC Sulfolobus.  
OX NCBI\_TaxID=2287;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-33.  
RC STRAIN=ATCC 49255 / DSM 5833 / MT-4;  
RX MEDLINE=91033070; PubMed=2121622;  
RA Cubellis M.V., Rozzo C., Montecuchi P., Rossi M.,  
RT "Isolation and sequencing of a new beta-galactosidase-encoding  
RL archaeobacterial gene.";  
RL Gene 94:89-94(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=98/2;  
RX MEDLINE=99315783; PubMed=10383958;  
RA Haebelstine C., Montalvo-Rodriguez R., Bini B., Carl A., Blum P.,  
RT "Coordinate transcripitional control in the hyperthermophilic archaeon  
RT Sulfolobus solfataricus.";  
RL J. Bacteriol. 181:3920-3927(1999).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 35092 / DSM 1617 / P2;  
RX MEDLINE=21332296; PubMed=11427726;  
RA She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,  
RA Aweyer M.J., Chan-Weher C.C.-Y., Clausen I.G., Curtis B.A.,  
RA De Moors A., Erasmo G., Fletcher C., Gordon P.M.K.,  
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,  
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,  
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,  
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.,  
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).  
RC STRAIN=ATCC 49255 / DSM 5833 / MT-4;  
RX MEDLINE=97446327; PubMed=9299327;  
RA Aguilar C.F., Sanderson I., Moracci M., Ciaramella M., Nucci R.,  
RA Rossi M., Pearl L.H.;  
RT "Crystal structure of the beta-glycosidase from the hyperthermophilic  
RT archaeon Sulfolobus solfataricus: resilience as a key factor in  
RT thermostability.";  
RL J. Mol. Biol. 271:789-802(1997).  
CC -1- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-  
CC galactose residues in beta-D-galactosides.  
CC -1- SUBUNIT: Homotetramer.  
CC -1- SIMILARITY: Belongs to family 1 of glycosyl hydrolases.  
CC -----  
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CC -----  
DR EMBL: M34696; AAA72843.1; -.  
DR EMBL: AF133036; AAD21094.1; -.  
DR EMBL: AE006893; AAK3121.1; -.  
DR PIR: B90483; B90483.  
DR PIR: JQ0767; JQ0767.  
DR PDB: 1GOW; 20-AUG-97.  
DR InterPro: IPR001360; Glyco\_hydro\_1.  
DR Pfam: PF00232; Glyco\_hydro\_1; 1.  
DR PRINTS: PR00131; GLHYDRLASE1.  
DR ProDom: PD000650; Glyco\_hydro\_1; 1.  
DR PROSITE: PS00572; GLYCOSYL\_HYDROL\_F1\_1; 1.  
DR PROSITE: PS00653; GLYCOSYL\_HYDROL\_F1\_2; 1.  
KW Hydrolase; Glycosidase; 3D-structure; Complete proteome.  
FT ACT\_SITE 206 206 PROTON DONOR (POTENTIAL).  
FT ACT\_SITE 387 387 NUCLEOPHILE (BY SIMILARITY).  
FT CONFLICT 235 235 A -> H (IN REF. 1).  
FT STRAND 2 3  
FT TURN 6 7  
FT STRAND 9 13  
FT HELIX 16 19  
FT TURN 21 22  
FT TURN 24 25  
FT STRAND 31 31  
FT HELIX 32 36  
FT TURN 37 38  
FT HELIX 40 44  
FT TURN 45 46  
FT HELIX 53 55  
FT TURN 59 61  
FT HELIX 63 72  
FT TURN 73 74  
FT STRAND 77 81  
FT HELIX 84 87  
FT TURN 100 101  
FT HELIX 112 118  
FT TURN 119 121  
FT HELIX 124 140  
FT TURN 141 141  
FT STRAND 143 143  
FT STRAND 154 154  
FT HELIX 155 157  
FT STRAND 158 158  
FT HELIX 160 164  
FT TURN 165 166  
FT STRAND 172 172  
FT HELIX 173 175  
FT HELIX 177 194  
FT TURN 195 197  
FT STRAND 200 205

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FT HELIX 207 215
FT TURN 216 220
FT HELIX 218 229
FT HELIX 229 253
FT STRAND 258 269
FT HELIX 272 274
FT HELIX 275 285
FT TURN 286 295
FT HELIX 297 302
FT STRAND 301 302
FT STRAND 303 306
FT TURN 308 312
FT TURN 317 330
FT TURN 331 332
FT STRAND 333 336
FT TURN 341 342
FT TURN 346 347
FT STRAND 349 352
FT TURN 351 352
FT STRAND 355 356
FT TURN 358 359
FT STRAND 362 362
FT TURN 365 365
FT HELIX 366 379
FT STRAND 383 387
FT HELIX 398 414
FT TURN 415 416
FT STRAND 419 425
FT STRAND 428 428
FT HELIX 433 438
FT STRAND 444 447
FT TURN 448 451
FT STRAND 452 455
FT HELIX 457 466
FT TURN 467 469
FT STRAND 470 471
FT HELIX 473 475
FT TURN 476 477
FT TURN 485 486
SO SEQUENCE 489 AA; 56691 MW; B56P6CE8E8A4A29D CRC64;

Query Match 54.7%; Score 35; DB 1; Length 489;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 YDPLTKW 9
Db 369 YDPLTKW 376

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RESULT 73
BACE_HUMAN
ID BACE_HUMAN STANDARD; PRT; 501 AA.
AC P56817; Q9BYB9; Q9BYC0; Q9BYC1; Q9UJ75;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Beta-secretase precursor (BC 3.4.23.46) (Beta-site APP cleaving
  enzyme) (beta-site amyloid precursor protein cleaving enzyme)
DE (Aspartyl) protease 2 (Asp 2) (ASP2) (Membrane-associated aspartic
  protease 2) (Memapsin-2).
DE BACE OR BACE1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=Brain;
RX MEDLINE=20002972; PubMed=10531052;
RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
  Denis P., Teplow D.B., Ross S., Amarante P., Loefloft R., Luo Y.,

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RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
RA Treanor J., Rogers G., Cilton M.,
RT "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
  the transmembrane aspartic protease BACE.",
RL Science 286:735-741(1999).
[2]
RP SEQUENCE FROM N.A. (ISOFORM A), SEQUENCE OF 46-68, AND
RP CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=20057171; PubMed=10591214;
RA Sinha S., Anderson J.P., Barbour R., Basi G.S., Caccavello R.,
RA Davis D., Doan M., Dovey H.F., Prignon N., Hong J., Jacobson-Croak K.,
RA Jewett N., Keim P., Knops J., Lieberburg I., Power M., Tan H.,
RA Tatsuno G., Tung J., Schenk D., Seubert P., Suemasa S.M., Wang S.,
RA Walker D., Zhao J., McConlogue L., Varghese J.,
RT "Purification and cloning of amyloid precursor protein beta-secretase
  from human brain.",
RL Nature 402:537-540(1999).
[3]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=20057170; PubMed=10591213;
RA Yan R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,
RA Brashler J.R., Strachan N.C., Mathews W.R., Buhl A.E., Carter D.B.,
RA Tomaseelli A.G., Parodi L.A., Heinrikson R.L., Gurey M.E.,
RT "Membrane-anchored aspartyl protease with Alzheimer's disease beta-
  secretase activity.",
RL Nature 402:533-537(1999).
[4]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=20120043; PubMed=10656250;
RA Hussain I., Powell D.V., Howlett D.R., Tew D.G., Meek T.D.,
RA Chapman C., Glover I.S., Murphy K.E., Southan C.D., Ryan D.M.,
RA Smith T.S., Simmons D.L., Walsh P.S., Dingwall C., Christie G.,
RT "Identification of a novel aspartic proteinase (Asp 2) as beta-
  secretase.",
RL Mol. Cell. Neurosci. 14:419-427(1999).
[5]
RP SEQUENCE FROM N.A. (ISOFORM B).
RC TISSUE=Brain, and Pancreas;
RA Michel B., De Pietri Tonelli D., Zaccchetti D., Keller P.,
RT "New beta-site APP cleaving enzyme isoform (BACE-1B) obtained from
  human brain and pancreas.",
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
[6]
RP SEQUENCE FROM N.A. (ISOFORM C).
RC TISSUE=Pancreas;
RA Zaccchetti D., De Pietri Tonelli D., Schnurbus R.,
RT "New beta-site APP cleaving enzyme isoform (BACE-1C) obtained from
  human pancreas.",
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
[7]
RP SEQUENCE FROM N.A. (ISOFORMS B; C AND D).
RC TISSUE=Brain;
RX MEDLINE=21408467; PubMed=11516562;
RA Tanahashi H., Tabira T.,
RT "Three novel alternatively spliced isoforms of the human beta-site
  amyloid precursor protein cleaving enzyme (BACE) and their effect on
  amyloid beta-peptide production.",
RL Neurosci. Lett. 307:9-12(2001).
[8]
RP SEQUENCE OF 14-501 FROM N.A. (ISOFORM A), AND CHARACTERIZATION.
RX MEDLINE=20144060; PubMed=10677483;
RA Lin X., Koelsch G., Wu S., Downs D., Dashti A., Tang J.,
RT "Human aspartic protease memapsin 2 cleaves the beta-secretase site of
  beta-amyloid precursor protein.",
RL Proc. Natl. Acad. Sci. U.S.A. 97:1456-1460(2000).
[9]
RP DISULFIDE BONDS.
RX MEDLINE=21950860; PubMed=11953458;
RA Fischer F., Molinari M., Bodendorf U., Paganetti P.,
RT "The disulphide bonds in the catalytic domain of BACE are critical but
  not essential for amyloid precursor protein processing activity.",

```



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DR EMBL: AF190726; AAF04144.1; -  
 DR EMBL: AF200346; AAF17082.1; -  
 DR HSSP: P56272; IAMS.  
 DR MEROPS: A01.004; -  
 DR MGI: MGI:1346542; Bace.  
 DR InterPro: IPR001969; Asprotease\_AS.  
 DR InterPro: IPR009007; Pept\_A\_acid.  
 DR InterPro: IPR001461; Peptidase\_A1.  
 DR Pfam: PF00026; asp. 1.  
 DR PRINTS: PR00792; PEPsin.  
 DR PROSITE: PS00141; ASP\_PROTEASE; 1.  
 DR Hydroxylase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;  
 KW Signal.  
 FT SIGNAL 1 21  
 FT PROPEP 22 45  
 FT CHAIN 46 501  
 FT DOMAIN 22 457  
 FT TRANSMEM 458 478  
 FT DOMAIN 479 501  
 FT ACT\_SITE 93 93  
 FT ACT\_SITE 289 289  
 FT DISULFID 216 420  
 FT DISULFID 278 443  
 FT CARBOHYD 153 153  
 FT CARBOHYD 172 172  
 FT CARBOHYD 223 223  
 FT CARBOHYD 354 354  
 SQ SEQUENCE 501 AA; 55747 MW; C085A013145E474E CRC64;

Query Match 54.7%; Score 35; DB 1; Length 501;  
 Best Local Similarity 44.4%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9  
 DB 250 WYTPIRREW 258

RESULT 75  
 BACE RAT STANDARD; PRT; 501 AA.  
 AC P56819;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Beta-secretase precursor (BC 3.4.23.46) (Beta-site APP cleaving  
 DE enzyme) (Beta-site amyloid precursor protein cleaving enzyme)  
 DE (Aspartyl) protease 2 (Asp 2) (ASP2) (Membrane-associated aspartic  
 DE protease 2) (Memapsin-2).  
 GN BACE.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=20002972; PubMed=10531052;  
 RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,  
 RA Denis P., Teplow D.B., Ross S., Amarante P., Lojoff R., Luo Y.,  
 RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,  
 RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,  
 RA Treanor J., Rogers G., Citron M.,  
 RA "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by  
 RA the transmembrane aspartic protease BACE".  
 RL Science 286:735-741(1999).  
 CC -1- FUNCTION: Responsible for the proteolytic processing of the  
 CC amyloid precursor protein (App). Cleaves at the amino terminus of

CC the A-beta peptide sequence, between residues 671 and 672 of App,  
 CC leads to the generation and extracellular release of beta-cleaved  
 CC soluble APP, and a corresponding cell-associated carboxy-terminal  
 CC fragment which is later release by gamma-secretase (By  
 CC similarity).

CC -1- CATALYTIC ACTIVITY: Broad endopeptidase specificity. Cleaves Glu-  
 CC Val-Asn-Leu-I-Asp-Ala-Glu-Phe in the Swedish variant of  
 CC Alzheimer's amyloid precursor protein.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Belongs to peptidase family A1.

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DR EMBL: AF190727; AAF04144.1; -  
 DR HSSP: P32329; IYPS.  
 DR MEROPS: A01.004; -  
 DR InterPro: IPR001969; Asprotease\_AS.  
 DR InterPro: IPR009007; Pept\_A\_acid.  
 DR InterPro: IPR001461; Peptidase\_A1.  
 DR Pfam: PF00026; asp. 1.  
 DR PRINTS: PR00792; PEPsin.  
 DR PROSITE: PS00141; ASP\_PROTEASE; 1.  
 DR Hydroxylase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;  
 KW Signal.  
 FT SIGNAL 1 21  
 FT PROPEP 22 45  
 FT CHAIN 46 501  
 FT DOMAIN 22 457  
 FT TRANSMEM 458 478  
 FT DOMAIN 479 501  
 FT ACT\_SITE 93 93  
 FT ACT\_SITE 289 289  
 FT DISULFID 216 420  
 FT DISULFID 278 443  
 FT CARBOHYD 153 153  
 FT CARBOHYD 172 172  
 FT CARBOHYD 223 223  
 FT CARBOHYD 354 354  
 SQ SEQUENCE 501 AA; 55806 MW; 24B445BC8B87DB3 CRC64;

Query Match 54.7%; Score 35; DB 1; Length 501;  
 Best Local Similarity 44.4%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9  
 DB 250 WYTPIRREW 258

RESULT 76  
 YAB4 MYCPN STANDARD; PRT; 524 AA.  
 AC P75609;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Hypothetical lipoprotein MPN084 precursor (R02\_crf524).  
 GN MPN084 OR MP071.  
 OS Mycoplasma pneumoniae.  
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
 OX NCBI\_TaxID=2104;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 29342 / M129;  
 RX MEDLINE=97105885; PubMed=8948633;  
 RA Himmelfreich R., Hilbert H., Plogens H., Pirkl E., Li B.-C.,

RA Herrmann R.;  
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma  
 RL pneumoniae";  
 CC Nucleic Acids Res. 24:4420-4449 (1996).  
 CC  
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor  
 CC (Potential).  
 CC  
 CC -1- SIMILARITY: BELONGS TO THE MG067 / MG068 / MG395 FAMILY.  
 CC  
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 CC  
 CC -----  
 CC DR EMBL; AE000009; AAB95719.1; -.  
 CC DR PIR; S73397; S73397.  
 CC DR InterPro; IPR009003; Cys Ser trypsin.  
 CC DR InterPro; IPR002414; DUF30/31.  
 CC DR Pfam; PF01727; DUF30.1.  
 CC DR Pfam; PF01732; DUF31.1.  
 CC DR PRINTS; PR00840; Y06768FAMILY.  
 CC DR Hypothetical protein; Lipoprotein; Membrane; Signal;  
 CC KW Complete proteome; Palmitate.  
 CC  
 CC FT SIGNAL 1 21 POTENTIAL.  
 CC FT CHAIN 1 524 HYPOTHETICAL LIPOPROTEIN MPN084.  
 CC FT LIPID 22 22 N-palmitoyl cysteine (Potential).  
 CC FT LIPID 22 22 S-diacylglycerol cysteine (Potential).  
 CC SQ SEQUENCE 524 AA; 59553 MW; F4E7138D8092E74F CRC64;  
 CC  
 CC Query Match 54.7%; Score 35; DB 1; Length 524;  
 CC Best Local Similarity 75.0%; Pred. No. 1.8e+02;  
 CC Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 CC  
 CC Oy 2 YDPLTKLM 9  
 CC Db 174 YDSLTKQW 181  
 CC  
 CC RESULT 77  
 CC Y469 HUMAN STANDARD; PRT; 539 AA.  
 CC ID Y469 HUMAN STANDARD; PRT; 539 AA.  
 CC AC Q9U9F4; O75057; 16-OCT-2001 (Rel. 40, Created)  
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 CC DT 16-OCT-2001 (Rel. 42, Last annotation update)  
 CC DE Hypothetical protein KIAA0469.  
 CC GN KIAA0469.  
 CC OS Homo sapiens (Human).  
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 CC OX NCBI\_TaxID=9606;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RC TISSUE=Brain;  
 CC RX MEDLINE=9811662; PubMed=9455484;  
 CC RA Seki N., Ohira M., Nagase T., Ishikawa K.-I., Miyajima N.,  
 CC RA Nakajima D., Nomura N., Ohara O.;  
 CC RT "Characterization of cDNA clones in size-fractionated cDNA libraries  
 CC from human brain.";  
 CC RL DNA Res. 4:345-349 (1997).  
 CC RN [2]  
 CC RP SEQUENCE FROM N.A.  
 CC RA Wray P.;  
 CC RT Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.  
 CC CC -1- SIMILARITY: Contains 1 BTB/POZ domain.  
 CC CC -1- SIMILARITY: Contains 5 Kelch repeats.  
 CC  
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 CC  
 CC -----  
 CC DR EMBL; AB007938; BA42314.1; -.  
 CC DR EMBL; AL031447; CAB42892.1; -.  
 CC DR InterPro; IPR000210; BTB POZ.  
 CC DR InterPro; IPR006652; Kelch\_rep.  
 CC DR Pfam; PF00651; BTB; 1.  
 CC DR Pfam; PF01344; Kelch; 5.  
 CC DR SMART; SM00225; BTB; 1.  
 CC DR SMART; SM00612; Kelch; 3.  
 CC DR PROSITE; PS50097; BTB; 1.  
 CC KW Hypothetical protein; Kelch repeat; Repeat.  
 CC  
 CC FT DOMAIN 35 103 BTB.  
 CC FT REPEAT 287 335 KELCH 1.  
 CC FT REPEAT 336 382 KELCH 2.  
 CC FT REPEAT 384 422 KELCH 3.  
 CC FT REPEAT 423 470 KELCH 4.  
 CC FT REPEAT 472 512 KELCH 5.  
 CC FT CONFLICT 534 534 D -> G (IN REF. 2).  
 CC SQ SEQUENCE 539 AA; 60435 MW; DDE88D184C077945 CRC64;  
 CC  
 CC Query Match 54.7%; Score 35; DB 1; Length 539;  
 CC Best Local Similarity 75.0%; Pred. No. 1.9e+02;  
 CC Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 CC  
 CC Oy 2 YDPLTKLM 9  
 CC Db 441 YDPDTLW 448  
 CC  
 CC RESULT 78  
 CC YEDQ\_ECO57 STANDARD; PRT; 564 AA.  
 CC ID YEDQ\_ECO57 STANDARD; PRT; 564 AA.  
 CC AC O8XB92;  
 CC DT 28-FEB-2003 (Rel. 41, Created)  
 CC DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 CC DE Hypothetical protein yedQ.  
 CC GN YEDQ OR Z3047 OR EC52694.  
 CC OS Escherichia coli O157:H7.  
 CC OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC OC Enterobacteriaceae; Escherichia.  
 CC OX NCBI\_TaxID=83334;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RC STRAIN=O157:H7 / EDL933 / ATCC 700927;  
 CC RX MEDLINE=21074935; PubMed=11206551;  
 CC RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,  
 CC RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
 CC RA Postal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
 CC RA Grobbeck E.J., Davis N.W., Lam A., Dimmler B.T., Potamousis K.,  
 CC RA Apodaca J., Anantharaman T.S., Iln J., Yen G., Schwartz D.C.,  
 CC RA Welch R.A., Blattner F.R.;  
 CC RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";  
 CC RL Nature 409:529-533 (2001).  
 CC RN [2]  
 CC RP SEQUENCE FROM N.A.  
 CC RC STRAIN=O157:H7 / RIMD 0509952;  
 CC RX MEDLINE=21156231; PubMed=11258796;  
 CC RA Hayaishi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
 CC RA Han C.-G., Ohtsundo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
 CC RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,  
 CC RA Kunihara S., Shiba T., Hattori M., Shinagawa H.;  
 CC RT "Complete genome sequence of enterohaemorrhagic Escherichia coli  
 CC O157:H7 and genomic comparison with a laboratory strain K-12.";  
 CC RL DNA Res. 8:11-23 (2001).  
 CC RN [3]  
 CC RP SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC CC -1- SIMILARITY: BELONGS TO THE YABC / YFIN (E.COLI), YHCK (B.SUBTILIS)  
 CC CC -1- SIMILARITY: Contains 1 GGDEF domain.  
 CC



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DR EMBL; AE005417; AAG56970.1; -  
DR EMBL; AP002559; BAB36117.1; -  
DR PIR; P90965; P90965.  
DR InterPro; IPR00160; GDEF.  
DR Pfam; PF00990; GDEF.1.  
DR SMART; SM00267; DUF1.1.  
DR TIGRFAMs; TIGR00254; GDEF.1.  
DR PROSITE; PS00887; GDEF.1.  
KW Hypothetical protein; Transmembrane; Complete proteome.  
FT TRANSMEM 20 40 POTENTIAL.  
FT TRANSMEM 360 380 POTENTIAL.  
FT DOMAIN 428 563 GDEF.  
SQ SEQUENCE 564 AA; 64287 MW; BBBC2286ADBAECB0 CRC64;

Query Match 54.7%; Score 35; DB 1; Length 564;  
Best Local Similarity 55.6%; Pred. No. 1.9e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYDFLTFLW 9  
Db 399 WHDTLRLY 407

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RESULT 79
YEDO_ECOLI STANDARD; PRT; 564 AA.
AC P76330; P94746;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein yedQ.
YEDO OR B1956.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.D.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=9725158; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasei H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA Mizubuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Samped G., Seki Y.,
RA Sivasubdam S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
[3]
RP SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1 SIMILARITY: BELONGS TO THE YABC / YFIN (B.COLI), YHCK (B.SUBTILIS)
CC FAMILY.
CC -1 SIMILARITY: Contains 1 GDEF domain.
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DR EMBL; AE000287; AAC75022.1; ALT\_INT.  
DR EMBL; D90835; BAA15784.1; -  
DR Ecocore; EG14040; yedQ.  
DR InterPro; IPR00160; GDEF.  
DR Pfam; PF00990; GDEF.1.  
DR SMART; SM00267; DUF1.1.  
DR TIGRFAMs; TIGR00254; GDEF.1.  
DR PROSITE; PS00887; GDEF.1.  
KW Hypothetical protein; Transmembrane; Complete proteome.  
FT TRANSMEM 20 40 POTENTIAL.  
FT TRANSMEM 360 380 POTENTIAL.  
FT DOMAIN 428 563 GDEF.  
SQ SEQUENCE 564 AA; 64283 MW; 05FB02C1BE2A938 CRC64;

Query Match 54.7%; Score 35; DB 1; Length 564;  
Best Local Similarity 55.6%; Pred. No. 1.9e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYDFLTFLW 9  
Db 399 WHDTLRLY 407

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RESULT 80
MIS_BOVIN STANDARD; PRT; 575 AA.
AC P03972;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Muellerian inhibiting factor precursor (MIS) (Anti-muellerian hormone)
DE (AMH) (muellerian inhibiting substance).
CN AMH.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
[1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=86218082; PubMed=3754790;
RA Cate R.L., Mataliano R.J., Hession C., Tizard R., Farber N.M.,
RA Cheung A., Ninfa E.G., Frey A.Z., Gash D.J., Chow E.P., Fisher R.A.,
RA Bercowski J.M., Torres G., Wallner B.P., Ramachandran K.L.,
RA Ragin R.C., Manganaro T.F., McLaughlin D.L., Donahoe P.K.;
RT "Isolation of the bovine and human genes for Mullerian inhibiting
RT substance and expression of the human gene in animal cells.";
RL Cell 45:685-698(1986).
[2]
RP FUNCTION: THIS GLYCOPROTEIN, PRODUCED BY THE SERTOLI CELLS OF THE
RP TESTIS, CAUSES REGRESSION OF THE MUELLERIAN DUCT. IT ALSO IS ABLE
RP TO INHIBIT THE GROWTH OF TUMORS DERIVED FROM TISSUES OF MUELLERIAN
RP DUCT ORIGIN.
CC -1 SUBUNIT: Homodimer; disulfide-linked.
CC -1 MISCELLANEOUS: Although it does not compete with EGF for receptor
CC binding sites, MIS can inhibit the autophosphorylation of the EGF
CC receptor in vitro.
CC -1 SIMILARITY: Belongs to the TGF-beta family.
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BROAD-SPECTRUM PEROXIDASE ACTIVITIES. MAY PLAY A ROLE IN THE  
INTRACELLULAR SURVIVAL OF MYCOBACTERIA (BY SIMILARITY).  
-1- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.  
-1- COFACTOR: Binds 1 heme b (iron-protoporphyrin IX) group per  
dimer.  
-1- SUBUNIT: Homodimer (probable).  
-1- SIMILARITY: Belongs to the peroxidase family. Bacterial  
peroxidase/catalase subfamily.  
-----  
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-----  
DR EMBL; Y07665; CAA69192.1; -.  
DR HSSP; P00431; 1CCK.  
DR InterPro; IPR000763; Bac. ctase/prase.  
DR InterPro; IPR002016; Peroxidase.  
DR Pfam; PF00141; Peroxidase; 1.  
DR PRINTS; PRO0458; PEROXIDASE.  
DR TIGRfam; TIGR00198; cat per HPI; 1.  
DR PROSITE; PS00435; PEROXIDASE\_1; 1.  
DR PROSITE; PS00436; PEROXIDASE\_2; 1.  
DR PROSITE; PS00873; PEROXIDASE\_4; 1.  
DR OXidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.  
FT ACT\_SITE 113 113 BY SIMILARITY.  
FT ACT\_SITE 117 117 BY SIMILARITY.  
FT METAL 285 285 IRON (HEM AXIAL LIGAND).  
SQ SEQUENCE 752 AA; 83100 MW; B66BAD53DD6E70D CRC64;  
  
Query Match 54.7%; Score 35; DB 1; Length 752;  
Best Local Similarity 55.6%; Pred. No. 2.6e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
Cy 2 YDPLTKLML 10  
Db 403 YGPIRRL 411  
  
RESULT 83  
ID KHL5 HUMAN STANDARD; PRT; 755 AA.  
AC Q96PQ7; O86XW0; Q9NUR3; Q9N27; Q9NVA9; Q9YX2;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 15-MAR-2004 (Rel. 43, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Kelch-like protein 5.  
OS Homo sapiens (Human).  
GN Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RC TISSUE=Fetal brain;  
RC MEDLINE=21474935; PubMed=11590829.  
RA Wang S., Zhou Z., Ying K., Tang R., Huang Y., Wu C., Xie Y., Mao Y.;  
RT "Cloning and characterization of KHL5, a novel human gene encoding a  
kelch-related protein with a BTB domain.";  
RL Biochem. Genet. 39:227-238(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Waterston R.H.;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 212-755 FROM N.A. (ISOFORM 1), AND SEQUENCE OF 476-755  
RC TISSUE=Placenta;  
RA Isegawa T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
RA Nishikawa T., Nagai K., Sugano S., Shitatori A., Sudo H.,

RA Magatsuna M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,  
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
RA Yamamoto K., Wakamatsu A., Nakamura Y., Nagahari K., Maeno Y.,  
RA Nimomura K., Iwayanagi T.;  
RT "NEO human cDNA sequencing project.";  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 383-755 FROM N.A. (ISOFORM 1).  
RC TISSUE=uterus;  
RA MEDLINE=22388257; PubMed=12477932;  
RA Strussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner K.H., Shemen C.M., Schluter G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang Y., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman W., Madan A., Rodriguez S., Sanchez A.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butcherfield A.S.N., Krzywinski M.I., Skalski U., Smalins D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [5]  
RP SEQUENCE OF 490-755 FROM N.A. (ISOFORM 3).  
RC TISSUE=tongue;  
RA Jiyi Y., Lianxian C., Zhengjian Z., Bo Y.;  
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- ALTERNATIVE PRODUCTS.  
CC Name=1;  
CC IsoId=Q96PQ7-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q96PQ7-2; Sequence=VSP\_008619;  
CC Note= May be due to intron retention. No experimental  
CC confirmation available;  
CC Name=3;  
CC IsoId=Q96PQ7-3; Sequence=VSP\_008620;  
CC Note=No experimental confirmation available;  
CC -1- TISSUE SPECIFICITY: Expressed in adrenal gland, ovary and thyroid  
CC gland and less abundantly in lymph node, prostate, spinal chord,  
CC testis and trachea.  
CC -1- SIMILARITY: Contains 1 BTB/POZ domain.  
CC -1- SIMILARITY: Contains 6 Kelch repeats.  
CC -1- CAUTION: Ref.1 (AAU08584) sequence differs from that shown due to  
CC a stop codon in position 735 which was translated as Trp to extend  
CC the sequence.  
-----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
DR EMBL; AF272976; AAL08584.1; ALT\_TERM.  
DR EMBL; AC079921; -; NOT ANNOTATED CDS.  
DR EMBL; AK001698; BAA91845.1; ALT\_INIT.  
DR EMBL; AK001836; BAA91933.1; ALT\_INIT.  
DR EMBL; AK002174; BAA92121.1; ALT\_INIT.  
DR EMBL; BC048262; AHA48262.1; -;  
DR EMBL; AF123320; AAD32565.1; ALT\_INIT.  
DR EMBL; HGNC:6356; KHL5.  
DR Genew; 608064; -;

```

DR GO: GO:0005737; C:cytoplasm; ISS.
DR GO: GO:0003779; P:actin binding; ISS.
DR GO: GO:0030036; P:actin cytoskeleton organization and biogenesis; ISS.
DR InterPro: IPR000210; BTB_P2.
DR InterPro: IPR006651; Kelch.
DR InterPro: IPR006652; Kelch_rep.
DR Pfam: PF00651; BTB; 1.
DR Pfam: PF01344; Kelch; 6.
DR PRINTS: PR00501; KELCHREPEAT.
DR SMART: SM00225; BTB; 1.
DR SMART: SM00612; Kelch; 6.
DR PROSITE: PS50097; BTB; 1.
KW Cytoskeleton; Actin-binding; Repeat; Kelch repeat;
Alternative splicing.
FT DOMAIN 220 287 BTB.
FT REPEAT 468 514 KELCH 1.
FT REPEAT 515 561 KELCH 2.
FT REPEAT 563 608 KELCH 3.
FT REPEAT 609 655 KELCH 4.
FT REPEAT 657 708 KELCH 5.
FT REPEAT 709 754 KELCH 6.
FT VARSPLIC 739 755 APLCGRAGACVTVTKL -> WHSCFIITLTLFLKQPLW
(in isoform 2).
FT VARSPLIC 739 755 /FTID=VSP_008619.
FT VARSPLIC 739 755 APLCGRAGACVTVTKL -> FSHTFEDSKHLVAIKQTIV
(RONSLSSEFRSH (in isoform 3)).
FT VARSPLIC 739 755 /FTID=VSP_008620.
FT CONFLICT 10 10 I -> L (IN REF. 1).
FT CONFLICT 323 323 L -> P (IN REF. 3; BAA91845).
FT CONFLICT 435 435 Q -> R (IN REF. 1).
FT CONFLICT 594 594 M -> K (IN REF. 3; BAA91845).
FT CONFLICT 695 695 S -> G (IN REF. 3; BAA92121).
SQ SEQUENCE 755 AA; 84457 MW; 2AB1BF98F387F6C CRC64;

Query Match 54.7%; Score 35; DB 1; Length 755;
Best Local Similarity 62.5%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9
DB 681 YDPKTDWM 688

RESULT 84
ID 41_XENLA STANDARD; PRT; 801 AA.
AC P11434;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytoskeletal protein 4.1 (Band 4.1).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
NC NCB1_TaxID=8355;
RN NCB1 [1]
RX MEDLINE=90249600; PubMed=2186944;
RA Spencer M., Giebelhaus D.H., Kelly G.M., Bicknell J., Florio S.K.,
RA Bunt-Milam A., Moon R.T.;
RA "Membrane skeleton protein 4.1 in developing Xenopus: expression in
RT postmitotic cells of the retina.";
RL Dev. Biol. 139:279-291(1990).
[2]
RN NCB1 [1]
RX MEDLINE=88223353; PubMed=2453290;
RA Giebelhaus D.H., Eib D.W., Moon R.T.;
RA "Antisense RNA inhibits expression of membrane skeleton protein 4.1
RT during embryonic development of Xenopus.";
RL Cell 53:601-615(1988).
CC -1- FUNCTION: Protein 4.1 is a major structural element of the
erythrocyte membrane skeleton. It plays a key role in regulating

```

```

CC membrane physical properties of mechanical stability and
CC deformability by stabilizing spectrin-actin interaction. Binds
CC with a high affinity to glycophorin and with lower affinity to
CC band III protein.
CC -1- TISSUE SPECIFICITY: Found exclusively in photoreceptors following
CC the terminal mitosis of retinal neurons. When retinal
CC synaptogenesis is complete, protein 4.1 is also expressed in the
CC inner retina. In adult amphibian retinas, protein 4.1 is detected
CC in photoreceptors, bipolar cells, and ganglion cell axons.
CC -1- PTM: Phosphorylated at multiple sites by different protein kinases
CC and each phosphorylation event selectively modulates the protein's
CC functions.
CC -1- SIMILARITY: Contains 1 FERM domain.
CC -----
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CC -----
CC EMBL: M20621; AAA49695.1; -.
CC PIR: A37353; A37353.
CC InterPro: IPR008379; 4_1_CTD.
CC InterPro: IPR000299; Band_4.1.
CC InterPro: IPR007477; SAB.
CC Pfam: PF05902; 4_1_CTD; 1.
CC Pfam: PF00373; Band_4.1; 1.
CC Pfam: PF04382; SAB; 1.
CC PRINTS: PR00935; BAND4.1.
CC SMART: SM00295; B41; 1.
CC PROSITE: PS00660; FERM_1; 1.
CC PROSITE: PS00661; FERM_2; 1.
CC PROSITE: PS50057; FERM_3; 1.
KW Structural protein; Cytoskeleton; Actin-binding; Phosphorylation.
FT DOMAIN 193 474 FERM.
FT DOMAIN 477 587 HYDROPHILIC.
FT DOMAIN 588 651 SPECTRIN-ACTIN-BINDING.
FT DOMAIN 653 801 CARBOXYL-TERMINAL (CTD).
SQ SEQUENCE 801 AA; 89429 MW; 07FA508552359A0F CRC64;

Query Match 54.7%; Score 35; DB 1; Length 801;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
DB 239 WESPCKVWL 248

RESULT 85
ID DMSA_RHOSH STANDARD; PRT; 822 AA.
AC O5736;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Dimethyl sulfoxide reductase precursor (EC 1.8.99.-) (DMSO reductase)
DE (DMSOR).
CN DMSA OR DSRA.
OS Rhodospirillum rubrum (Rhodospirillum rubrum).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacteriales;
OC Rhodobacteraceae; Rhodobacter.
NC NCB1_TaxID=1063;
RN NCB1 [1]
RX MEDLINE=9624838; PubMed=8645727;
RA Hilton J.C., Rajagopalan K.V.;
RA "Molecular cloning of dimethyl sulfoxide reductase from Rhodobacter
RT sphaeroides.";
RL Biochim. Biophys. Acta 1294:111-114(1996).

```

[2] SEQUENCE FROM N.A., SEQUENCE OF N-TERMINUS, AND PARTIAL SEQUENCE.  
RP STRAIN-11106;  
RX MEDLINE=96068928; PubMed=8534974;  
RA Yamamoto I., Wada N., Ujiye T., Tachibana M., Matsuzaki M.,  
RT Kajiwara H., Watanabe Y., Hirano H., Okubo A., Satoh T., Yamazaki S.,  
RT "Cloning and nucleotide sequence of the gene encoding dimethyl  
RT sulfoxide reductase from Rhodospirillum rubrum F. sp.  
RT dehydrificans".  
RU Biochem. Biotechnol. 59:1850-1855(1995).  
[3]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RX MEDLINE=96247313; PubMed=8658134;  
RA Schindelin H., Kisker C., Hilton J., Rajagopalan K.V., Rees D.C.,  
RT "Crystal structure of DMSO reductase: redox-linked changes in  
RT molybdopterin coordination."  
RU Science 272:1615-1621(1996).  
[4]  
RP X-RAY CRYSTALLOGRAPHY (1.3 ANGSTROMS).  
RA Li H.-K., Temple C., Rajagopalan K.V., Schindelin H.,  
RT "The 1.3 A crystal structure of Rhodospirillum rubrum dimethyl  
RT sulfoxide reductase reveals two distinct molybdenum coordination  
RT environments."  
RU J. Am. Chem. Soc. 122:7673-7680(2000).  
CC -I- FUNCTION: Terminal reductase during anaerobic growth on  
CC various sulfoxide and N-oxide compounds.  
CC -I- CATALYTIC ACTIVITY: Reduces various N-oxide and sulfoxide  
CC compounds including trimethylamine N-oxide.  
CC -I- COFACTOR: Molybdenum (molybdopterin).  
CC -I- SUBUNIT: Monomer.  
CC -I- SUBCELLULAR LOCATION: Periplasmic.  
CC -I- PTM: Predicted to be exported by the Tat system. The position of  
CC the signal peptide cleavage has been experimentally proven.  
CC -I- SIMILARITY: Belongs to the prokaryotic molybdopterin-containing  
CC oxidoreductase family.  
-----  
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DR EMBL: LA6851; AAB07230.1; -  
DR EMBL: D38634; BAA07615.1; -  
DR PIR: S70012; S70012.  
DR PDB: 1E01; 03-OCT-01.  
DR InterPro: IPR009010; Asp decarb\_fold.  
DR InterPro: IPR006658; Biac.  
DR InterPro: IPR006657; Mol dinuc bind.  
DR InterPro: IPR006656; Molybdopterin.  
DR InterPro: IPR006655; Prok Mboxred.  
DR InterPro: IPR006311; Tat.  
DR Pfam: PF00384; molybdopterin; 1.  
DR Pfam: PF01568; Molybdop binding; 1.  
DR TIGRfam: TIGR00509; biac fam; 1.  
DR TIGRfam: TIGR01409; Tat signal seq; 1.  
DR PROSITE: PS00551; MOLYBDOPTERIN\_PROK\_1; FALSE\_NEG.  
DR PROSITE: PS00490; MOLYBDOPTERIN\_PROK\_2; 1.  
DR PROSITE: PS00932; MOLYBDOPTERIN\_PROK\_3; 1.  
KM Oxidoreductase; Molybdenum; Periplasmic; Signal; 3D-structure.  
FT SIGNAL 1 42  
FT CHAIN 43 822  
FT ACT SITE 189 189  
FT STRAND 48 54  
FT TURN 55 56  
FT STRAND 57 64  
FT TURN 65 66  
FT STRAND 67 73  
FT TURN 75 76  
FT TURN 82 83  
FT HELIX 84 89

FT TURN 90 92  
FT TURN 94 95  
FT STRAND 96 96  
FT STRAND 101 103  
FT HELIX 104 109  
FT HELIX 110 112  
FT HELIX 115 117  
FT TURN 118 119  
FT STRAND 123 125  
FT HELIX 128 146  
FT HELIX 148 150  
FT STRAND 151 152  
FT HELIX 167 178  
FT TURN 179 179  
FT STRAND 182 185  
FT TURN 191 192  
FT HELIX 193 200  
FT TURN 201 201  
FT TURN 206 207  
FT HELIX 213 219  
FT STRAND 222 226  
FT HELIX 230 233  
FT TURN 234 235  
FT STRAND 240 240  
FT HELIX 244 244  
FT TURN 256 256  
FT STRAND 258 262  
FT STRAND 265 265  
FT HELIX 268 273  
FT TURN 274 274  
FT STRAND 276 278  
FT TURN 282 283  
FT HELIX 285 298  
FT TURN 299 300  
FT HELIX 304 310  
FT STRAND 311 312  
FT HELIX 321 321  
FT TURN 322 326  
FT HELIX 332 339  
FT HELIX 343 354  
FT STRAND 358 362  
FT HELIX 365 367  
FT TURN 370 372  
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FT TURN 387 387  
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FT TURN 403 406  
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FT TURN 458 459  
FT STRAND 469 463  
FT STRAND 473 473  
FT HELIX 477 480  
FT HELIX 484 490  
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FT STRAND 503 503  
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FT STRAND 513 517  
FT STRAND 520 522  
FT HELIX 525 529  
FT TURN 531 533  
FT STRAND 536 540  
FT TURN 548 549  
FT STRAND 551 551  
FT HELIX 553 563

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FT TURN 564 565
FT HELIX 567 571
FT TURN 572 573
FT HELIX 576 583
FT TURN 594 595
FT HELIX 601 607
FT STRAND 609 611
FT HELIX 616 619
FT TURN 622 623
FT HELIX 624 628
FT TURN 630 632
FT TURN 638 639
FT STRAND 642 643
FT HELIX 647 652
FT TURN 655 656
FT TURN 670 671
FT TURN 673 674
FT STRAND 679 682
FT STRAND 690 690
FT TURN 691 692
FT STRAND 693 693
FT TURN 694 696
FT HELIX 702 702
FT TURN 703 703
FT STRAND 705 705
FT TURN 706 707
FT STRAND 708 708
FT STRAND 710 713
FT HELIX 715 719
FT TURN 720 722
FT TURN 725 726
FT STRAND 728 732
FT STRAND 737 744
FT TURN 746 747
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Query Match 54.7%; Score 35; DB 1; Length 822;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WYDPL 5  
Db 760 WYDPL 764

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RESULT 86
EF2_BETVU STANDARD; PRT; 843 AA.
AC 023755;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor 2 (EF-2).
OS Beta vulgaris (Sugar beet).
OC Eubacteriales; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Beta.
OX NCBI_TaxID=161934;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Root;
RA Vogel R.; Rausch T.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: This protein promotes the GTP-dependent translocation of
CC the nascent protein chain from the A-site to the P-site of the
CC ribosome.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: Phosphorylation by EF-2 kinase completely inactivates EF-2
CC (By similarity).
CC -1- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC EF-G/EF-2 subfamily.
CC -----
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DR EMBL; Z97178; CAB09900.1; -.
DR PIR; T14579; T14579.
DR InterPro; IPR000795; EF_GTPbind.
DR InterPro; IPR000640; EFG_C.
DR InterPro; IPR009022; EFG_III_V.
DR InterPro; IPR005517; EFG_IV_.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR009000; Translat_factor.
DR Pfam; PF00679; EFG_C_1.
DR Pfam; PF03764; EFG_IV_1.
DR Pfam; PF00009; GTP_EFTU_1.
DR Pfam; PF03144; GTP_EFTU_D2_1.
DR PRINTS; PR00315; ELONGATNFACT.
DR PROSITE; PS00301; EFACROR_GTP_1.
KM Elongation factor; GTP-binding; Protein biosynthesis; Phosphorylation.
FT NP_BIND 26 33 GTP (BY SIMILARITY).
FT NP_BIND 104 108 GTP (BY SIMILARITY).
FT NP_BIND 158 161 GTP (BY SIMILARITY).
FT MOD_RES 57 57 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 59 59 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 700 700 DIPHTHAMIDE (BY SIMILARITY).
SQ SEQUENCE 843 AA; 93799 MW; D11325B42A51F4F8 CRC64;
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Query Match 54.7%; Score 35; DB 1; Length 843;  
Best Local Similarity 55.6%; Pred. No. 2.9e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 WYDPLTKLM 9  
Db 249 FPDPAKKM 257

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RESULT 87
POL_MPMV STANDARD; PRT; 867 AA.
AC P07572;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE POL polypeptide (Contains: Reverse transcriptase (EC 2.7.7.49);
DE Endonuclease).
GN POL.
OS Simian Mason-Pfizer virus (MPV).
OC Viruses; Retroid viruses; Retroviridae; Betaretrovirus.
OX NCBI_TaxID=11855;
RN [1]
RP SEQUENCE FROM N.A. (CLONE 6A).
RX MEDLINE=86189951; PubMed=2421920;
RA Sonigo P.; Barker C.; Hunter E.; Main-Hobson S.;
RT "Nucleotide sequence of Mason-Pfizer monkey virus: an
RT immunosuppressive D-type retrovirus.";
RL Cell 45:375-385(1986).
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {DNA} (N).
CC -1- Specific enzymatic cleavages in vivo yield mature proteins.
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CC EMBL; M12349; AAA47711.1; -.
CC PIR; C25839; GNLMJP.
CC HSPB; P03355; IMWL.
```

DR InterPro; IPR001037; Integrase\_C.  
 DR InterPro; IPR003308; Integrase\_Zn.  
 DR InterPro; IPR002156; RNaseH.  
 DR InterPro; IPR001584; Rve.  
 DR InterPro; IPR000477; RVTse.  
 DR Pfam; PF00552; Integrase\_1.  
 DR Pfam; PF02022; Integrase; 1.  
 DR Pfam; PF00075; RNaseH; 1.  
 DR Pfam; PF00665; rve; 1.  
 DR Pfam; PF00078; rvt; 1.  
 DR Transferrase; RNA-directed DNA polymerase; Hydrolase; Nuclease;  
 KW Endonuclease; Polypeptide.  
 SQ SEQUENCE 867 AA; 98404 MW; 0F5EDPC7B997935 CRC64;

Query Match 54.7%; Score 35; DB 1; Length 867;  
 Best Local Similarity 55.6%; Pred. No. 3e+02;  
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 WYDPLTKLM 9  
 DB 816 WKDPLDNTW 824

RESULT 88  
 ID POL\_SRV1 STANDARD; PRT; 867 AA.  
 AC P04025;  
 DT 23-OCT-1996 (Rel. 02, Created)  
 DT 23-OCT-1996 (Rel. 02, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE POL polyprotein [Contains: Reverse transcriptase (EC 2.7.7.49);  
 DE Endonuclease].  
 GN POL.  
 OS Simian retrovirus SRV-1.  
 CC Viruses; Retrovirdae; Betaretrovirus.  
 OC NCBI\_TaxID=11942;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86151668; PubMed=3006247;  
 RA Power M.D., Marx P.A., Bryant M.L., Gardner M.B., Barr P.J.,  
 RA Luciw P.A.;  
 RT Nucleotide sequence of SRV-1, a type D simian acquired immune  
 RT deficiency syndrome retrovirus.;  
 RL Science 231:1567-1572(1986).  
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate  
 + [DNA] (N).  
 CC -1- PTM: Specific enzymatic cleavages in vivo yield mature proteins.  
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 CC -----  
 DR EMBL; M1841; AAA4732.1; -  
 DR HSSP; P03355; 1MWL.  
 DR InterPro; IPR001037; Integrase\_C.  
 DR InterPro; IPR003308; Integrase\_Zn.  
 DR InterPro; IPR002156; RNaseH.  
 DR InterPro; IPR001584; Rve.  
 DR InterPro; IPR000477; RVTse.  
 DR Pfam; PF00552; Integrase\_1.  
 DR Pfam; PF02022; Integrase; 1.  
 DR Pfam; PF00075; RNaseH; 1.  
 DR Pfam; PF00665; rve; 1.  
 DR Pfam; PF00078; rvt; 1.  
 DR Transferrase; RNA-directed DNA polymerase; Hydrolase; Nuclease;  
 KW Endonuclease; Polypeptide.  
 SQ SEQUENCE 867 AA; 98361 MW; ABB06A0B770A6473 CRC64;

Query Match 54.7%; Score 35; DB 1; Length 867;

Best Local Similarity 55.6%; Pred. No. 3e+02;  
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 WYDPLTKLM 9  
 DB 816 WKDPLDNTW 824

RESULT 89  
 ID POL\_SRV2 STANDARD; PRT; 867 AA.  
 AC P51517;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE POL polyprotein [Contains: Reverse transcriptase (EC 2.7.7.49);  
 DE Endonuclease].  
 GN POL.  
 OS Simian retrovirus SRV-2.  
 CC Viruses; Retrovirdae; Betaretrovirus.  
 OC NCBI\_TaxID=39068;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87151131; PubMed=2435057;  
 RA Thayer R.M., Power M.D., Bryant M.L., Gardner M.B., Barr P.J.,  
 RA Luciw P.A.;  
 RT "Sequence relationships of type D retroviruses which cause simian  
 RT acquired immunodeficiency syndrome.";  
 RL Virology 157:317-329(1987).  
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate  
 + [DNA] (N).  
 CC -1- PTM: Specific enzymatic cleavages in vivo yield mature proteins.  
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 CC -----  
 DR EMBL; M16605; AAA47562.1; -  
 DR HSSP; P03355; 1MWL.  
 DR InterPro; IPR001037; Integrase\_C.  
 DR InterPro; IPR003308; Integrase\_Zn.  
 DR InterPro; IPR002156; RNaseH.  
 DR InterPro; IPR001584; Rve.  
 DR InterPro; IPR000477; RVTse.  
 DR Pfam; PF00552; Integrase\_1.  
 DR Pfam; PF02022; Integrase; 1.  
 DR Pfam; PF00075; RNaseH; 1.  
 DR Pfam; PF00665; rve; 1.  
 DR Pfam; PF00078; rvt; 1.  
 DR Transferrase; RNA-directed DNA polymerase; Hydrolase; Nuclease;  
 KW Endonuclease; Polypeptide.  
 SQ SEQUENCE 867 AA; 98038 MW; F64227F7365F3659 CRC64;

Query Match 54.7%; Score 35; DB 1; Length 867;  
 Best Local Similarity 55.6%; Pred. No. 3e+02;  
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9  
 DB 816 WKDPLDNTW 824

RESULT 90  
 ID UAKI\_MOUSE STANDARD; PRT; 1153 AA.  
 AC P53332; O62126;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Tyrosine-protein kinase JAK1 (EC 2.7.1.112) (Janus kinase 1) (JAK-1).  
 GN JAK1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93322747; PubMed=8331382;  
 RA Yang X., Chung D., Cepko C.L.;  
 RT "Molecular cloning of the murine JAK1 protein tyrosine kinase and its  
 RT expression in the mouse central nervous system."; J. Neurosci. 13:3006-3017(1993).  
 RL [2]  
 RN SEQUENCE OF 999-1069 FROM N.A.  
 RP MEDLINE=90152381; PubMed=2482828;  
 RA Wilks A.F., Kurban R.R., Hovens C.M., Ralph S.J.;  
 RT "The application of the polymerase chain reaction to cloning members  
 RT of the protein tyrosine kinase family."; Gene 85:67-74(1989).  
 RL [3]  
 RN SEQUENCE OF 999-1069 FROM N.A.  
 RP MEDLINE=89160824; PubMed=2465296;  
 RA Wilks A.F.;  
 RT "Two putative protein-tyrosine kinases identified by application of  
 RT the polymerase chain reaction."; Proc. Natl. Acad. Sci. U.S.A. 86:1603-1607(1989).  
 RL [1]  
 CC FUNCTION: Tyrosine kinase of the non-receptor type, involved in  
 CC the TNF-alpha/beta/gamma signal pathway. Kinase partner for the  
 CC interleukin (IL)-2 receptor.  
 CC [1]  
 CC CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC [1]  
 CC SUBCELLULAR LOCATION: Wholly intracellular, possibly membrane  
 CC associated.  
 CC [1]  
 CC DOMAIN: Possesses two phosphotransferase domains. The second one  
 CC probably contains the catalytic domain (By similarity), while the  
 CC presence of slight differences suggest a different role for domain  
 CC 1.  
 CC [1]  
 CC SIMILARITY: Belongs to the Tyr family of protein kinases. JAK  
 CC subfamily.  
 CC [1]  
 CC SIMILARITY: Contains 1 SH2 domain.  
 CC [1]  
 CC SIMILARITY: Contains 1 FERM domain.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: S63728; AAB27517.2; -;  
 CC EMBL: M33425; AAA40016.1; -;  
 CC HSSP: P11362; IFGK.  
 CC MGD: MGI:96628; Jak1.  
 CC InterPro: IPR0000299; Band 4.1.  
 CC InterPro: IPR000719; Prot\_Kinase.  
 CC InterPro: IPR000980; SH2.  
 CC InterPro: IPR001245; Tyr\_kinase.  
 CC InterPro: IPR008266; Tyr\_pkinase\_AS.  
 CC Pfam: PF00069; Pkinase; 2.  
 CC Pfam: PF00017; SH2; 1.  
 CC PRINTS: PR00109; TYRKINASE.  
 CC PRODOM: PD000001; Prot\_Kinase; 2.  
 CC PRODOM: PD000093; SH2; 1.  
 CC SMART: SMO0295; B41; 1.  
 CC SMART: SMO0252; SH2; 1.  
 CC SMART: SMO0219; Tyrc; 1.  
 CC PROSITE: PS00660; FERM\_1; FALSE NEG.  
 CC PROSITE: PS00661; FERM\_2; FALSE NEG.  
 CC PROSITE: PS00507; FERM\_3; 1.  
 CC PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 CC PROSITE: PS00011; PROTEIN\_KINASE\_DOM; 2.

DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS00001; SH2; 1.  
 KM Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;  
 GN SH2 domain; Repeat.  
 FT DOMAIN 34 420 FERM.  
 FT DOMAIN 334 362 HIGHLY CHARGED.  
 FT DOMAIN 439 528 SH2 (ATYPICAL).  
 FT DOMAIN 582 854 PROTEIN KINASE 1.  
 FT DOMAIN 874 1152 PROTEIN KINASE 2.  
 FT NP\_BIND 880 888 ATP (BY SIMILARITY).  
 FT BINDING 907 907 ATP (BY SIMILARITY).  
 FT ACT\_SITE 1002 1002 BY SIMILARITY.  
 FT MOD\_RES 1033 1033 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT CONFLICT 999 999 V->I (IN REF. 2 AND 3).  
 FT CONFLICT 1068 1069 VT->IP (IN REF. 2 AND 3).  
 SQ SEQUENCE 1153 AA; 133367 MW; 0B9816A5B3868B CRC64;  
 Query Match 54.7%; Score 35; DB 1; Length 1153;  
 Best Local Similarity 75.0%; Pred. No. 4e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 YDPLTKLM 9  
 DB 81 YDESTKLM 88  
 RESULT 91  
 ID KIELC\_DROME STANDARD; PRT; 1477 AA.  
 AC 004652; Q04653; Q86PA7; Q9VJA2;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ring canal Kieich protein [Contains: Kieich short protein].  
 GN KIEL OR CG7210.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RX MEDLINE=93201592; PubMed=8453663;  
 RA Xue F., Cooley L.;  
 RT "Kieich encodes a component of intercellular bridges in Drosophila egg  
 RT chambers."; Cell 72:681-693(1993).  
 RL Cell 72:681-693(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Holskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richardson S., Ashburner M., Henderson S.N.,  
 RA Sutton R.G., Wortman W.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfaffler B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,  
 RA Burtis K.C., Busam D.A., Butler H., Caden E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodex A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jaiswal M., Kalish F., Karen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merklow G., Mishina N.V., Mohanty C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Stryker R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye U., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of *Drosophila melanogaster*,"  
 RT Science 287:2185-2195(2000).  
 RN [3]  
 RP REVISIONS.  
 RX MEDLINE=22426069; PubMed=12537572;  
 RA Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.B.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
 RA Bertencourt B.R., Celinker S.B., de Grey A.D.N.J., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.,  
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
 RT systematic review,"  
 RL Genome Biol. 3:RESEARCH0083.22(2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley; TISSUE=Embryo;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.W.,  
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
 RA George R.A., Gonzalez M., Guarin H., Krommiller B. L. P.W., Liao G.,  
 RA Miranda A., Mungall C.J., Nunco J., Pacleb J.M., Parasas V., Park S.,  
 RA Patel S., Phouanavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celinker S.E.;  
 RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 RL [5]  
 RP CHARACTERIZATION.  
 RC TISSUE=Embryo;  
 RX MEDLINE=97236487; PubMed=9118811;  
 RA Robinson D.N., Cooley L.;  
 RT "Examination of the function of two kelch proteins generated by stop  
 RT codon suppression,"  
 RL Development 124:1405-1417(1997).  
 CC -!- FUNCTION: Component of ring canals that regulates the flow of  
 CC cytoplasm between cells. May be involved in the regulation of  
 CC cytoplasm flow from nurse cells to the oocyte during oogenesis.  
 CC Binds actin.  
 CC -!- SUBCELLULAR LOCATION: Inner surface of cytoplasmic bridges or ring  
 CC canals present in egg chambers. Subcortically in imaginal disk  
 CC epithelia.  
 CC -!- TISSUE SPECIFICITY: Both proteins are expressed in ovaries: male  
 CC testis, ovariectomized females, cuticle, salivary gland and  
 CC imaginal disks. Kelch short protein is the predominant form and  
 CC is also expressed in fat bodies. On entry into metamorphosis  
 CC levels of full length protein increase in testis and imaginal  
 CC disks.  
 CC -!- DEVELOPMENTAL STAGE: Larvae, pupae and adults.  
 CC -!- SIMILARITY: Contains 1 BTB/POZ domain.  
 CC -!- SIMILARITY: Contains 6 Kelch repeats.  
 CC -!- CAUTION: Ref.5 believes residue 690 is a selenocysteine.  
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CC -----  
 DR EMBL; L08483; AAA53471.1; -  
 DR EMBL; L08483; AAA53472.2; -  
 DR EMBL; AE003657; AAF53651.1; -  
 DR EMBL; AE003657; AAF53651.2; -  
 DR EMBL; BT003250; AA025007.1; ALT\_SEQ.  
 DR HSSP; 005516; IC93.  
 DR FlyBase; FBgn000301; kel.  
 DR GO; GO:0007292; P:female gamete generation; IMP.  
 DR GO; GO:0007301; P:ovarian ring canal formation; IDA.  
 DR InterPro; IPR000210; BTB\_POZ.  
 DR InterPro; IPR006651; Kelch.  
 DR InterPro; IPR006652; Kelch\_rep.  
 DR Pfam; PF00651; BTB, 1.  
 DR Pfam; PF01344; Kelch, 6.  
 DR PRINTS; PR00501; KELCHREPEAT.  
 DR SMART; SM00225; BTB, 1.  
 DR SMART; SM00612; Kelch, 6.  
 DR PROSITE; PS50097; BTB, 1.  
 KW Cytoskeleton; Actin-binding; Selenium; Selenocysteine; Kelch repeat;  
 KW Repeat.  
 FT CHAIN 1 1477  
 FT CHAIN 1 689  
 FT DOMAIN 157 223  
 FT REPEAT 404 449  
 FT REPEAT 450 496  
 FT REPEAT 498 543  
 FT REPEAT 545 592  
 FT REPEAT 594 639  
 FT REPEAT 641 687  
 FT DOMAIN 18 28  
 FT DOMAIN 29 87  
 FT DOMAIN 29 36  
 FT DOMAIN 78 83  
 FT SE\_CYS 690 690  
 FT CONFLICT 493 493  
 FT CONFLICT 596 596  
 FT CONFLICT 824 824  
 FT CONFLICT 858 858  
 FT CONFLICT 1083 1083  
 FT CONFLICT 1086 1086  
 SQ SEQUENCE 1477 AA; 160086 MW; 4851EEAE999DBA47 CRC64;  
 Query Match 54.7%; Score 35; DB 1; Length 1477;  
 Best Local Similarity 62.5%; Pred. NO. 5.2e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 YDPLTKW 9  
 Db 516 YDPKTDIW 523  
 RESULT 92  
 ID UBL1\_KLUA STANDARD; PRT; 1941 AA.  
 AC 060014;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE N-end-recognizing protein (Ubl1qutin-protein ligase E3 component) (N-  
 DE recognin).  
 GN UBL1.  
 OS Kluyveromyces fragilis (Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.  
 OX NCBI\_TaxID=28995;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Waller P.R.H., Varshavsky A.;  
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Recognition component of the N-end rule pathway. Binds  
 CC to proteins bearing amino-terminal residues that are destabilizing  
 CC according to the N-end rule, but does not bind to otherwise



identical proteins bearing stabilizing amino-terminal residues.  
-1- SIMILARITY: Contains 1 UBR1-type zinc finger.  
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-----  
DR EMBL; AF061554; AAC15841.1; -  
DR PIR; T30554; T30554.  
DR InterPro; IPR003126; Znf\_Nrecoznln.  
DR InterPro; IPR001841; Znf\_Tring.  
DR Pfam; PF02207; ZF-UBR1; 1.  
DR SMART; SM00184; RING; 1.  
DR SMART; SM00396; Znf\_UBR1; 1.  
DR Ligase; Ubl conjugation pathway.  
KW SEQUENCE 1941 AA; 223682 MW; 37C2E1BCA0803268 CRC64;  
Query Match 54.7%; Score 35; DB 1; Length 1941;  
Best Local Similarity 55.6%; Pred. No. 6.9e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
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QY 2 YDPLTKML 10  
DB 1748 YEHLRLMI 1756  
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RESULT 93  
Y960\_HAEIN STANDARD; PRT; 116 AA.  
AC P44084;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Hypothetical protein H10960 precursor.  
GN H10960.  
OS Haemophilus influenzae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
OC Pasteurellaceae; Haemophilus.  
OX NCBI\_TaxID=727;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=Rd / KM20 / ATCC 51907;  
RX MEDLINE=95350630; PubMed=7542800;  
RA Fleisemann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
RA Scott J.D., Shirley R., Liu L.-I., Glodex A., Kelley J.M.,  
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom B., Cotton M.D.,  
RA Utechtack T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,  
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
RA Venter J.C.;  
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae  
RT Rd.";  
RL Science 269:496-512(1995).  
-----  
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-----  
DR EMBL; U32777; AAC22628.1; -  
DR PIR; C64017; C64017.  
DR TIGR; H10960; -  
DR InterPro; IPR000437; Prok\_Lipoprot\_S.  
DR PROSITE; PS00013; PROKAR\_LIPOPROTEIN; UNKNOWN\_1.

Hypothetical protein; Signal; Complete proteome.  
FT SIGNAL 1 15 POTENTIAL.  
FT CHAIN 16 116 HYPOTHETICAL PROTEIN H10960.  
SQ SEQUENCE 116 AA; 13498 MW; 97214FD32CE8C25F CRC64;  
Query Match 53.1%; Score 34; DB 1; Length 116;  
Best Local Similarity 54.5%; Pred. No. 57;  
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;  
-----  
QY 1 WYDPL--TKM 9  
DB 68 WYDHGVTOIW 78  
-----  
RESULT 94  
SP2G\_BACTK STANDARD; PRT; 161 AA.  
AC P26767;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Possible sporulation sigma factor processing peptidase (EC 3.4.23.-)  
DE (Fragment).  
OS Bacillus thuringiensis (subsp. kurstaki).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=29339;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=HD-1-Dippel;  
RX MEDLINE=91267951; PubMed=1904859;  
RA Adams L.F., Brown K.L., Whiteley H.R.;  
RT "Molecular cloning and characterization of two genes encoding sigma  
RT factors that direct transcription from a Bacillus thuringiensis  
RT crystal protein gene promoter.";  
RL J. Bacteriol. 173:3846-3854(1991).  
CC -1- FUNCTION: PROBABLY ACTIVATES THE RNA POLYMERASE SIGMA-35 FACTOR  
CC AT THE STAGE II OF SPOULATION.  
CC -1- SIMILARITY: TO B SUBTILIS SPOITGA.  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY U4. IT IS POSSIBLE THAT  
CC THIS IS AN ASPARTYL PROTEASE.  
-----  
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-----  
DR EMBL; X56697; CAA40025.1; -  
DR PIR; D39441; D39441.  
DR MEROPS; U04.001; -  
DR InterPro; IPR005081; Peptidase\_U4.  
DR Pfam; PF03419; Peptidase\_U4; 1.  
KW Sporulation; Hydrolase; Aspartyl protease.  
FT NON\_TER 1  
FT ACT\_SITE 38 38 BY SIMILARITY.  
SQ SEQUENCE 161 AA; 18182 MW; 09945F97F64FFBF CRC64;  
Query Match 53.1%; Score 34; DB 1; Length 161;  
Best Local Similarity 100.0%; Pred. No. 80;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
-----  
QY 2 YDPLTK 7  
DB 44 YDPLTK 49  
-----  
RESULT 95  
RNH2\_PYRAB STANDARD; PRT; 224 AA.  
ID RNH2\_PYRAB  
AC Q9VIA9;  
DT 16-OCT-2001 (Rel. 40, Created)

```

RT      "The complete sequence of the Pyrococcus furiosus genome." ;
RL      Submitted (FEB-2002) to the EMBL/genbank/DBJ databases.
CC      -1- FUNCTION: This enzyme is an endonuclease that degrades the RNA of
CC      RNA-DNA hybrids specifically (By similarity).
CC      -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
CC      phosphomonoester.
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC      -1- SIMILARITY: Belongs to the RNase HII family.
-----
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-----
DR      EMBL; AE010276; AAL81905.1; -.
DR      HAMAP; MF_00052; -.
DR      InterPro; IPR001352; RNase_HII/HIIT.
DR      InterPro; IPR004649; RNH1T.
DR      Pfam; PF01351; RNase_HII; 1.
DR      TIGRFAMs; TIGR00729; TIGR00729; 1.
DR      HydroBase; Nuclease; Complete proteome.
FT      ACT_SITE       7
FT      ACT_SITE       7
FT      ACT_SITE       105
FT      ACT_SITE       135
FT      ACT_SITE       BY SIMILARITY.
SQ      SEQUENCE        224 AA; 25315 MW; 6AAB6B6040E323F9 CRC64;
OY      3 DPLTKMWL 10
Db      173 DPKTKMWL 180

Query Match          53.1%; Score 34; DB 1; Length 224;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches    6; Conservative    0; Mismatches    2; Indels    0; Gaps    0;

RESULT 97
PRAA_RAT
ID      PRAA_RAT              STANDARD;             PRT;           227 AA.
AC      P09320;
DT      01-MAR-1989 (Rel. 10, Created)
DT      01-MAR-1989 (Rel. 10, Last sequence update)
DT      01-OCT-1994 (Rel. 30, Last annotation update)
DS      Placental prolactin-like protein A precursor (PLF-A).
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      MEDLINE=66278172; Pubmed=3755436;
RA      Duckworth M.L.; Peden L.M.; Friesen H.G.;
RT      "Isolation of a novel prolactin-like cDNA clone from developing rat
RT      placenta." ;
RU      U. Biol. Chem. 261:10879-10884(1986).
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- DEVELOPMENTAL STAGE: Expressed from days 14 to term of pregnancy.
CC      -1- SIMILARITY: Belongs to the somatotroph/prolactin family.
-----
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-----
DR      EMBL; M13750; AAA41890.1; -.
DR      PIR; A24911; A24911.
DR      HSSP; Q28632; LAN3.
InterPro; IPR001400; Somatotropin.

```

Query Match 53.1%; Score 34; DB 1; Length 243;

```
QY      3 DPLTKLWL 10
        |||||
Db     199 DPETKAWL 206
```

## RESULT 100

```

MOBD BPT4
ID MOBD BPT4 STANDARD; PRT; 259 AA.
AC P39241; 096216;
DT 01-FEB-1995 (Rel. 31, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable mobile endonuclease D.
GN MOBD OR TK.-10.
OS Bacteriophage T4.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=10665;
RN [1]
RP SEQUENCE FROM N.A.
RA Mzhavla N., Marusich E., Djavakhishvili T., Neitzel J., Peterson S.,
RA Awaya M., Eidemiller J., Canada D., Tracy J., Gailbreath K.,
RA Paddison P., Anderson B., Stidham T., Blattner F., Kutter E.M.;
RT "The 10.7 kb 'nonessential' region of bacteriophage T4 between the
RT genes tk and nrdC: twenty new t4 genes, generally conserved among
RT T-even phages."
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22514363; Pubmed=12626885;
RA Miller E.S., Kutter E., Mosig G., Arisaka F., Kunisawa T., Ruger W.;
RT "Bacteriophage T4 genome."
RL Microbiol. Mol. Biol. Rev. 67:86-156(2003).
CC -1- SIMILARITY: TO PHAGE T4 MOBB AND MOBC.
CC -----
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CC -----
DR EMBL: U76612; AAB26970.1; -.
DR EMBL: AF158101; AAD42592.1; -.
DR InterPro: IPR002711; HNH.
DR InterPro: IPR003615; HNH_nuc.
DR Pfam: PF01844; HNH_1.
DR SMART: SM00507; HNHc; 1.
DR SMART: SM00507; HNHc; 1.
KW Hydrolyase; Nuclease; Endonuclease.
SQ SEQUENCE 259 AA; 30453 MW; C149B7657EA138F4 CRC64;
Query Match 53.1%; Score 34; DB 1; Length 259;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 YDPLTKLWL 10
DB 207 YDLTKLWMI 215

```

Search completed: July 12, 2004, 21:27:44  
 Job time : 15 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 12, 2004, 21:22:37 ; Search time 39 Seconds

(without alignments)  
80.902 Million cell updates/sec

Title: US-09-932-613-457

Perfect score: 64

Sequence: 1 WYDPLTKML 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacterioplasmid:\*  
17: sp\_archaeoplasmid:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	73.4	291	16	Q98F87 rhizobium 1
2	46	71.9	766	6	Q9A1R8 ovine aries
3	45	71.9	870	15	Q7SME9 Q7SME9 enzootic na
4	45	70.3	383	10	Q9S102 Q9S102 arabis arabis
5	45	70.3	482	16	Q9KA06 Q9KA06 bacillus ha
6	43	67.2	538	5	Q9VGE5 Q9VGE5 drosophila
7	43	67.2	570	5	Q9VGE5 Q9VGE5 drosophila
8	43	67.2	575	5	Q9VGE5 Q9VGE5 drosophila
9	43	67.2	947	5	Q9VGE5 Q9VGE5 drosophila
10	43	67.2	947	5	Q9VGE5 Q9VGE5 drosophila
11	43	67.2	1218	5	Q9VGE5 Q9VGE5 drosophila
12	42	65.6	119	16	Q989U1 Q989U1 bradyrhizob
13	42	65.6	176	17	Q989U1 Q989U1 bradyrhizob
14	42	65.6	227	16	Q989U1 Q989U1 bradyrhizob
15	42	65.6	290	15	Q9YNA2 Q9YNA2 sheep pulmo
16	42	65.6	291	15	Q9YNA2 Q9YNA2 sheep pulmo

17	42	65.6	293	10	Q94A88 Q94A88 arabidopsis
18	42	65.6	374	10	Q81798 Q81798 arabidopsis
19	42	65.6	392	10	Q9SVA3 Q9SVA3 arabidopsis
20	42	65.6	442	12	Q91H17 Q91H17 discula des
21	42	65.6	619	4	Q9V480 Q9V480 homo sapien
22	42	65.6	641	4	Q9NZX0 Q9NZX0 homo sapien
23	42	65.6	642	4	Q9V6Y0 Q9V6Y0 homo sapien
24	42	65.6	873	6	Q9SNE6 Q9SNE6 ovine aries
25	42	65.6	874	15	Q9W7R3 Q9W7R3 sheep pulmo
26	41.5	64.8	312	10	Q9AYF3 Q9AYF3 oryza sativ
27	41.5	64.8	312	10	Q9AYF3 Q9AYF3 oryza sativ
28	41	64.1	144	2	Q9R7Z8 Q9R7Z8 vibrio chol
29	41	64.1	168	2	Q9R7Z8 Q9R7Z8 vibrio chol
30	41	64.1	309	16	Q98XCI Q98XCI laccobacill
31	41	64.1	514	10	Q8VMD8 Q8VMD8 lycopersico
32	41	64.1	539	16	Q8IV89 Q8IV89 bacillus an
33	41	64.1	539	16	Q8II13 Q8II13 bacillus ce
34	41	64.1	591	16	Q7VIF7 Q7VIF7 helicobacte
35	41	64.1	604	16	Q8A1Z5 Q8A1Z5 bacteroides
36	41	64.1	655	16	Q9KOR4 Q9KOR4 vibrio chol
37	41	64.1	672	16	Q910K3 Q910K3 pseudomonas
38	41	64.1	694	2	Q8L121 Q8L121 pseudomonas
39	41	64.1	733	16	Q7UTU4 Q7UTU4 rhodospirill
40	41	64.1	808	2	Q70021 Q70021 saccharopol
41	40	62.5	111	9	Q7Y308 Q7Y308 enterobacte
42	40	62.5	173	16	Q87XC5 Q87XC5 pseudomonas
43	40	62.5	230	5	Q817A3 Q817A3 plactyneris
44	40	62.5	345	2	Q9S180 Q9S180 salmonella
45	40	62.5	345	16	Q53933 Q53933 salmonella
46	40	62.5	378	10	Q9M2B5 Q9M2B5 arabidopsis
47	40	62.5	500	13	Q770Y2 Q770Y2 xenopus lae
48	40	62.5	513	5	Q9V8N4 Q9V8N4 drosophila
49	40	62.5	513	5	Q9V8N4 Q9V8N4 drosophila
50	40	62.5	519	16	Q9A9X4 Q9A9X4 cauliobacter
51	40	62.5	582	4	Q8N5C3 Q8N5C3 homo sapien
52	40	62.5	612	10	Q8SB55 Q8SB55 oryza sativ
53	40	62.5	612	10	Q7XFE5 Q7XFE5 oryza sativ
54	40	62.5	617	5	Q86BF1 Q86BF1 drosophila
55	40	62.5	620	5	Q81H99 Q81H99 drosophila
56	40	62.5	640	13	Q7ZVQ8 Q7ZVQ8 brachydanio
57	40	62.5	648	3	Q8J2J6 Q8J2J6 candida alb
58	40	62.5	713	10	Q8LM21 Q8LM21 oryza sativ
59	40	62.5	715	5	Q8IKX0 Q8IKX0 plasmodium
60	40	62.5	979	5	Q8IKX4 Q8IKX4 plasmodium
61	39.5	61.7	283	16	Q877F0 Q877F0 pseudomonas
62	39	60.9	109	12	Q91W3 Q91W3 hepatitis c
63	39	60.9	155	2	Q54791 Q54791 rhodobacter
64	39	60.9	158	2	Q9RCF8 Q9RCF8 rhodobacter
65	39	60.9	176	2	Q848N8 Q848N8 gamma-prote
66	39	60.9	177	6	Q9GLF8 Q9GLF8 trichosurus
67	39	60.9	240	16	Q9CFP6 Q9CFP6 pasteurilla
68	39	60.9	274	17	Q96YU1 Q96YU1 sulfolobus
69	39	60.9	335	10	Q9LYY7 Q9LYY7 arabidopsis
70	39	60.9	365	10	Q9T035 Q9T035 arabidopsis
71	39	60.9	403	5	Q9W3D5 Q9W3D5 drosophila
72	39	60.9	430	5	Q17702 Q17702 caenorhabdi
73	39	60.9	440	16	Q7UA40 Q7UA40 synecococc
74	39	60.9	480	5	Q17700 Q17700 caenorhabdi
75	39	60.9	518	16	Q86G73 Q86G73 pseudomonas
76	39	60.9	551	16	Q24953 Q24953 helicobacte
77	39	60.9	551	16	Q9ZMT9 Q9ZMT9 helicobacte
78	39	60.9	837	3	Q9HFR8 Q9HFR8 colicettric
79	39	60.9	848	16	Q8A3P6 Q8A3P6 bacteroides
80	39	60.9	871	6	Q9N172 Q9N172 trichosurus
81	39	60.9	941	6	Q9T7A5 Q9T7A5 bos taurus
82	39	60.9	948	16	Q8XX42 Q8XX42 ralestona s
83	39	60.9	2183	16	Q86585 Q86585 streptomyce
84	38.5	60.2	277	16	Q7UT29 Q7UT29 rhodospirill
85	38	59.4	33	2	F71125 F71125 campylobact
86	38	59.4	43	16	Q8FEY0 Q8FEY0 leprospira
87	38	59.4	92	10	Q8W3Q4 Q8W3Q4 silene noct
88	38	59.4	140	16	Q8EUP0 Q8EUP0 mycoplasma
89	38	59.4	190	16	Q9K9C7 Q9K9C7 bacillus ha

90	38	59.4	206	17	027482	027482 methanobact	163	37	57.8	346	10	091896	Q91896 chlorarachn
91	38	59.4	283	16	Q8A620	Q8A620 bacteroides	164	37	57.8	346	10	Q7X107	Q7X107 chlorarachn
92	38	59.4	295	5	016974	016974 caenothabdi	165	37	57.8	349	12	Q67775	Q67775 xanthomonas
93	38	59.4	300	5	Q9N3X5	Q9N3X5 caenothabdi	166	37	57.8	349	16	Q8P804	Q8P804 xanthomonas
94	38	59.4	302	4	081W46	081W46 homo sapien	167	37	57.8	355	2	Q91UW6	Q91UW6 escherichia
95	38	59.4	321	3	Q9P3R4	Q9P3R4 neurospora	168	37	57.8	355	16	Q9P0D4	Q9P0D4 ureaplasma
96	38	59.4	341	16	Q91072	Q91072 pseudomonas	169	37	57.8	357	16	Q922H2	Q922H2 rhizobium m
97	38	59.4	345	16	Q8BUT8	Q8BUT8 pseudomonas	170	37	57.8	390	16	Q87CM6	Q87CM6 xylella fas
98	38	59.4	361	16	Q8BUT8	Q8BUT8 pseudomonas	171	37	57.8	401	16	Q9ACN8	Q9ACN8 caulobacter
99	38	59.4	361	16	Q8BUT8	Q8BUT8 pseudomonas	172	37	57.8	427	13	Q803E6	Q803E6 brachydanio
100	38	59.4	362	10	Q8BUT8	Q8BUT8 pseudomonas	173	37	57.8	483	10	Q84JG7	Q84JG7 oryza sativ
101	38	59.4	380	10	Q80573	Q80573 aradidopsis	174	37	57.8	485	5	Q9NA31	Q9NA31 caenothabdi
102	38	59.4	453	11	Q8B280	Q8B280 mus musculu	175	37	57.8	494	5	Q01965	Q01965 caenothabdi
103	38	59.4	459	8	Q955T7	Q955T7 cheirogaleu	176	37	57.8	495	4	Q96G42	Q96G42 homo sapien
104	38	59.4	459	8	Q955T7	Q955T7 cheirogaleu	177	37	57.8	505	16	Q96H13	Q96H13 rhizobium 1
105	38	59.4	459	8	Q955T7	Q955T7 cheirogaleu	178	37	57.8	518	16	Q989V7	Q989V7 rhizobium 1
106	38	59.4	475	10	Q9LW55	Q9LW55 aradidopsis	179	37	57.8	536	10	Q947C2	Q947C2 gossypium a
107	38	59.4	485	16	Q8B280	Q8B280 mus musculu	180	37	57.8	542	5	Q9YVU2	Q9YVU2 drosophila
108	38	59.4	485	16	Q8B280	Q8B280 mus musculu	181	37	57.8	572	4	Q43J26	Q43J26 homo sapien
109	38	59.4	494	4	Q8N9B9	Q8N9B9 homo sapien	182	37	57.8	590	16	Q7UTF4	Q7UTF4 rhodospirell
110	38	59.4	503	16	Q8N9B9	Q8N9B9 homo sapien	183	37	57.8	603	16	Q8A878	Q8A878 bacteroides
111	38	59.4	512	10	Q9LV33	Q9LV33 aradidopsis	184	37	57.8	604	16	Q8A3N2	Q8A3N2 bacteroides
112	38	59.4	535	11	Q8BUI1	Q8BUI1 mus musculu	185	37	57.8	606	16	Q9X0N8	Q9X0N8 bacteroides
113	38	59.4	549	16	Q24952	Q24952 helicobacte	186	37	57.8	608	16	Q9X0B2	Q9X0B2 thermotoga
114	38	59.4	558	16	Q9ZMU0	Q9ZMU0 helicobacte	187	37	57.8	640	11	Q8K430	Q8K430 ratius norv
115	38	59.4	558	16	Q8NBE8	Q8NBE8 homo sapien	188	37	57.8	660	16	Q83055	Q83055 treponema p
116	38	59.4	568	11	Q8C840	Q8C840 mus musculu	189	37	57.8	743	8	Q8BNU0	Q8BNU0 pseudomonas
117	38	59.4	568	11	Q8C840	Q8C840 mus musculu	190	37	57.8	743	8	Q9XQJ7	Q9XQJ7 streptococ
118	38	59.4	625	4	Q96SY2	Q96SY2 homo sapien	191	37	57.8	812	4	Q86VU3	Q86VU3 homo sapien
119	38	59.4	625	4	Q96SY2	Q96SY2 homo sapien	192	37	57.8	814	16	Q8C79	Q8C79 escherichia
120	38	59.4	630	16	Q8D7L1	Q8D7L1 vibrio vuln	193	37	57.8	839	16	Q8C24	Q8C24 plasmodium 1
121	38	59.4	645	16	Q8RDB4	Q8RDB4 streptomyce	194	37	57.8	952	5	Q8IDU7	Q8IDU7 plasmodium 1
122	38	59.4	728	5	Q9VZ8	Q9VZ8 drosophila	195	37	57.8	965	4	Q8G35	Q8G35 escherichia
123	38	59.4	730	16	Q9WMS6	Q9WMS6 homo sapien	196	37	57.8	1105	16	Q8F310	Q8F310 escherichia
124	38	59.4	734	16	Q8AAM6	Q8AAM6 bacteroides	197	37	57.8	1288	17	Q96XW6	Q96XW6 sulfolobus
125	38	59.4	779	10	Q93Y21	Q93Y21 aradidopsis	198	37	57.8	1296	4	Q8TDS7	Q8TDS7 streptococ
126	38	59.4	803	17	Q97U8	Q97U8 sulfolobus	199	37	57.8	1416	4	Q8TDS7	Q8TDS7 streptococ
127	38	59.4	849	4	Q9N768	Q9N768 homo sapien	200	37	57.8	1416	4	Q8TDS7	Q8TDS7 streptococ
128	38	59.4	888	10	Q81225	Q81225 aradidopsis	201	37	57.8	222	16	Q9RR69	Q9RR69 delnoccocus
129	38	59.4	888	10	Q81225	Q81225 aradidopsis	202	37	57.8	222	16	Q9RR69	Q9RR69 delnoccocus
130	38	59.4	930	11	Q9ULC0	Q9ULC0 mus musculu	203	37	57.8	667	17	Q9R479	Q9R479 caenothabdi
131	38	59.4	964	4	Q9N771	Q9N771 homo sapien	204	37	57.8	723	16	Q8A279	Q8A279 caenothabdi
132	38	59.4	1045	4	Q9N771	Q9N771 homo sapien	205	37	57.8	723	16	Q8A279	Q8A279 caenothabdi
133	38	59.4	1071	4	Q7Z3C7	Q7Z3C7 homo sapien	206	37	57.8	74	12	Q8UW2	Q8UW2 white spot
134	38	59.4	1086	4	Q9P2P4	Q9P2P4 mus musculu	207	37	57.8	124	10	Q9S4Y4	Q9S4Y4 oryza sativ
135	38	59.4	1198	11	Q80T55	Q80T55 mus musculu	208	37	57.8	147	16	Q98B12	Q98B12 white spot
136	38	59.4	1769	4	Q9P273	Q9P273 mus musculu	209	37	57.8	170	13	Q7ZTW0	Q7ZTW0 oryza sativ
137	38	59.4	1822	2	Q8R6G6	Q8R6G6 chloroflexu	210	37	57.8	181	8	Q954J6	Q954J6 sarcitilthrip
138	38	59.4	1822	2	Q8R6G6	Q8R6G6 chloroflexu	211	37	57.8	181	8	Q954J6	Q954J6 sarcitilthrip
139	38	59.4	2144	4	Q9ULU2	Q9ULU2 mus musculu	212	37	57.8	209	11	Q819T5	Q819T5 sarcitilthrip
140	38	59.4	2144	4	Q9ULU2	Q9ULU2 mus musculu	213	37	57.8	209	11	Q819T5	Q819T5 sarcitilthrip
141	38	59.4	2144	4	Q9ULU2	Q9ULU2 mus musculu	214	37	57.8	209	11	Q819T5	Q819T5 sarcitilthrip
142	38	59.4	2144	4	Q9ULU2	Q9ULU2 mus musculu	215	37	57.8	209	11	Q819T5	Q819T5 sarcitilthrip
143	38	59.4	2144	4	Q9ULU2	Q9ULU2 mus musculu	216	37	57.8	209	11	Q819T5	Q819T5 sarcitilthrip
144	38	59.4	2144	4	Q9ULU2	Q9ULU2 mus musculu	217	37	57.8	209	11	Q819T5	Q819T5 sarcitilthrip
145	38	59.4	2144	4	Q9ULU2	Q9ULU2 mus musculu	218	37	57.8	209	11	Q819T5	Q819T5 sarcitilthrip
146	38	59.4	2144	4	Q9ULU2	Q9ULU2 mus musculu	219	37	57.8	209	11	Q819T5	Q819T5 sarcitilthrip
147	38	59.4	2144	4	Q9ULU2	Q9ULU2 mus musculu	220	37	57.8	209	11	Q819T5	Q819T5 sarcitilthrip
148	38	59.4	2144	4	Q9ULU2	Q9ULU2 mus musculu	221	37	57.8	209	11	Q819T5	Q819T5 sarcitilthrip
149	38	59.4	2144	4	Q9ULU2	Q9ULU2 mus musculu	222	37	57.8	209	11	Q819T5	Q819T5 sarcitilthrip
150	38	59.4	2144	4	Q9ULU2	Q9ULU2 mus musculu	223	37	57.8	209	11	Q819T5	Q819T5 sarcitilthrip
151	38	59.4	2144	4	Q9ULU2	Q9ULU2 mus musculu	224	37	57.8	209	11	Q819T5	Q819T5 sarcitilthrip
152	38	59.4	2144	4	Q9ULU2	Q9ULU2 mus musculu	225	37	57.8	209	11	Q819T5	Q819T5 sarcitilthrip
153	38	59.4	2144	4	Q9ULU2	Q9ULU2 mus musculu	226	37	57.8	209	11	Q819T5	Q819T5 sarcitilthrip
154	38	59.4	2144	4	Q9ULU2	Q9ULU2 mus musculu	227	37	57.8	209	11	Q819T5	Q819T5 sarcitilthrip
155	38	59.4	2144	4	Q9ULU2	Q9ULU2 mus musculu	228	37	57.8	209	11	Q819T5	Q819T5 sarcitilthrip
156	38	59.4	2144	4	Q9ULU2	Q9ULU2 mus musculu	229	37	57.8	209	11	Q819T5	Q819T5 sarcitilthrip
157	38	59.4	2144	4	Q9ULU2	Q9ULU2 mus musculu	230	37	57.8	209	11	Q819T5	Q819T5 sarcitilthrip
158	38	59.4	2144	4	Q9ULU2	Q9ULU2 mus musculu	231	37	57.8	209	11	Q819T5	Q819T5 sarcitilthrip
159	38	59.4	2144	4	Q9ULU2	Q9ULU2 mus musculu	232	37	57.8	209	11	Q819T5	Q819T5 sarcitilthrip
160	38	59.4	2144	4	Q9ULU2	Q9ULU2 mus musculu	233	37	57.8	209	11	Q819T5	Q819T5 sarcitilthrip
161	38	59.4	2144	4	Q9ULU2	Q9ULU2 mus musculu	234	37	57.8	209	11	Q819T5	Q819T5 sarcitilthrip
162	38	59.4	2144	4	Q9ULU2	Q9ULU2 mus musculu	235	37	57.8	209	11	Q819T5	Q819T5 sarcitilthrip

236	36	56.2	375	11	09CY38	09CY38 mus musculus
237	36	56.2	379	13	09NK28	09NK28 eptaretus
238	36	56.2	380	17	08TKM0	08TKM0 methanosarc
239	36	56.2	405	16	09PCF3	09PCF3 xylella fas
240	36	56.2	411	16	07VAS8	07VAS8 prochloroco
241	36	56.2	413	16	03V208	03V208 enterococu
242	36	56.2	416	11	0805V4	0805V4 mus musculu
243	36	56.2	418	10	08L991	08L991 arabidopsis
244	36	56.2	418	10	09M1Y1	09M1Y1 arabidopsis
245	36	56.2	419	2	046445	046445 chlamydia t
246	36	56.2	423	11	08BTG8	08BTG8 mus musculu
247	36	56.2	424	16	084654	084654 chlamydia t
248	36	56.2	427	16	083185	083185 shigella fl
249	36	56.2	429	11	08BSD9	08BSD9 mus musculu
250	36	56.2	432	16	0839E4	0839E4 enterococu
251	36	56.2	445	11	08CFJ4	08CFJ4 mus musculu
252	36	56.2	451	16	08FGT1	08FGT1 escherichia
253	36	56.2	459	8	09G3S7	09G3S7 pteropus sc
254	36	56.2	459	8	09G6M6	09G6M6 pteropus da
255	36	56.2	460	16	09PH40	09PH40 xylella fas
256	36	56.2	460	16	087E57	087E57 xylella fas
257	36	56.2	472	16	088QJ3	088QJ3 pseudomonas
258	36	56.2	473	16	08J0B2	08J0B2 neotrypanid
259	36	56.2	476	11	09R0J8	09R0J8 mus musculu
260	36	56.2	485	11	08BTM6	08BTM6 mus musculu
261	36	56.2	493	2	08GE77	08GE77 streptomyce
262	36	56.2	516	10	07XYP6	07XYP6 oryza sativ
263	36	56.2	531	5	0966P6	0966P6 caenorhabdi
264	36	56.2	531	5	061795	061795 caenorhabdi
265	36	56.2	540	5	P90787	P90787 caenorhabdi
266	36	56.2	571	11	09CR40	09CR40 mus musculu
267	36	56.2	589	13	07ZUA7	07ZUA7 xenopus lae
268	36	56.2	620	4	07Z330	07Z330 homo sapien
269	36	56.2	629	11	08C1U1	08C1U1 mus musculu
270	36	56.2	629	11	08CD84	08CD84 mus musculu
271	36	56.2	642	10	09S944	09S944 vitis vinif
272	36	56.2	642	11	099KN0	099KN0 mus musculu
273	36	56.2	642	11	092008	092008 mus musculu
274	36	56.2	652	5	081427	081427 plasmodium
275	36	56.2	654	11	08C706	08C706 mus musculu
276	36	56.2	691	11	08C7K3	08C7K3 mus musculu
277	36	56.2	713	5	09GV24	09GV24 sarcophaga
278	36	56.2	726	8	08HTM6	08HTM6 sinopodophy
279	36	56.2	726	8	08HTM8	08HTM8 diphylla
280	36	56.2	726	8	08HTM7	08HTM7 podophyllu
281	36	56.2	726	8	08HTM6	08HTM6 dysosma ple
282	36	56.2	728	16	08YMT0	08YMT0 arabidopsis
283	36	56.2	756	5	061224	061224 scypha raph
284	36	56.2	795	10	08LOJ1	08LOJ1 oryza sativ
285	36	56.2	795	17	08U2W5	08U2W5 pyrococcus
286	36	56.2	806	10	09FNA3	09FNA3 arabidopsis
287	36	56.2	808	4	09UFA3	09UFA3 homo sapien
288	36	56.2	954	4	096AY1	096AY1 homo sapien
289	36	56.2	954	4	09U193	09U193 homo sapien
290	36	56.2	954	4	09NZC9	09NZC9 homo sapien
291	36	56.2	1033	11	08K137	08K137 mus musculu
292	36	56.2	1036	11	08BW12	08BW12 mus musculu
293	36	56.2	1148	3	0031897	0031897 saccharomyc
294	36	56.2	1223	12	09INJ2	09INJ2 kadidiro vi
295	36	56.2	1249	12	065152	065152 african swi
296	36	56.2	1269	17	097206	097206 sulfobus
297	36	56.2	1292	3	09C163	09C163 rhizomucor
298	36	56.2	1328	11	08CHS5	08CHS5 mus musculu
299	36	56.2	1497	4	014997	014997 homo sapien
300	36	56.2	1803	11	09ESY1	09ESY1 ratus norv

## ALIGNMENTS

RESULT 1  
098FS7  
ID 098FS7  
PRELIMINARY:  
PRT: 291 AA.

AC	098FS7:	Query Match	73.4%	Score 47;	DB 16;	Length 291;
DT	01-OCT-2001 (TRENBLREL 18, Created)	Best Local Similarity	70.0%	Pred. No. 5.8;		
DT	01-OCT-2001 (TRENBLREL 18, Last sequence update)	Matches	7;	Conservative	1;	Mismatches 2; Indels 0; Gaps 0;
DE	01-MAR-2002 (TRENBLREL 20, Last annotation update)					
DE	Hypothetical protein mlr3636.					
GN	MLR3636.					
OS	Rhizobium loti (Mesorhizobium loti).					
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;					
OC	Phyllobacteriaceae; Mesorhizobium.					
OX	NCBI_TaxID=381;					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=MAFF030393;					
RX	MEDLINE=21082930; PubMed=11214968;					
RA	Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,					
RA	Watanabe A., Idekawa K., Ishikawa A., Kawashima K., Kimura T.,					
RA	Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,					
RA	Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,					
RA	Takeuchi C., Yamada M., Tabata S.,					
RT	"Complete genome structure of the nitrogen-fixing symbiotic bacterium					
RT	Mesorhizobium loti."					
RL	DNA Ref. 7:331-338 (2000).					
DR	EMBL; AP003002; BAB50490.1;					
KW	Hypothetical protein; Complete proteome.					
SEQUENCE	291 AA; 31162 MW; 36E651E33A79EE2 CRC64;					
RESULT 2						
ID	09NIR8	PRELIMINARY:	PRT: 766 AA.			
AC	09NIR8:					
DT	01-OCT-2000 (TRENBLREL 15, Created)					
DT	01-OCT-2000 (TRENBLREL 15, Last sequence update)					
DT	01-OCT-2003 (TRENBLREL 25, Last annotation update)					
DE	Pol.					
GN	Pol.					
OS	Ovis aries (Sheep).					
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;					
OC	Bovidae; Caprine; Ovis.					
OX	NCBI_TaxID=9940;					
RP	SEQUENCE FROM N.A.					
RC	MEDLINE=20392162; PubMed=10933716;					
RA	Palmarini M., Halliworth C., York D., Murgia C., de Oliveira T.,					
RA	Spencer T., Fan H.,					
RT	"Molecular cloning and functional analysis of three type D endogenous					
RT	retroviruses of sheep reveal a different cell tropism from that of the					
RT	highly related exogenous Jaagsiekte sheep retrovirus."					
RL	J. Virol. 74:8065-8076 (2000).					
DR	EMBL; AF153615; AAF29458.1;					
DR	GO; GO:0003677; F:DNA binding; IEA.					
DR	GO; GO:0008907; F:integrase activity; IEA.					
DR	GO; GO:0004523; F:ribonuclease H activity; IEA.					
DR	GO; GO:0003723; F:RNA binding; IEA.					
DR	GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.					
DR	GO; GO:0016740; F:transferase activity; IEA.					
DR	GO; GO:0008270; F:zinc ion binding; IEA.					
DR	GO; GO:0015074; P:DNA integration; IEA.					
DR	GO; GO:0006310; P:DNA recombination; IEA.					
DR	GO; GO:0006278; P:RNA dependent DNA replication; IEA.					
DR	InterPro; IPR001037; Integrase_Cn.					
DR	InterPro; IPR003308; Integrase_Zn.					
DR	InterPro; IPR002156; RNaseH.					
DR	InterPro; IPR001584; Rve.					

DR InterPro: IPR000477; RVTse.  
 DR Pfam: PF002022; Integrase\_2n; 1.  
 DR Pfam: PF000075; rnaaseh; 1.  
 DR Pfam: PF00665; rve; 1.  
 DR Pfam: PF00078; rvt; 1.  
 DR RNA-directed DNA polymerase; Transferase.  
 SQ SEQUENCE 766 AA; 86948 MW; 0CC13CCED56BE99 CRC64;

Query Match  
 Best Local Similarity 71.9%; Score 46; DB 6; Length 766;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Dr 1 WYDPLTKLW 9  
 720 WKDPLTNLW 728

## RESULT 3

07SWE9 PRELIMINARY; PRT; 870 AA.  
 AC 07SWE9; PRELIMINARY; PRT; 870 AA.  
 DT 01-OCT-2003 (TREMBLrel. 25, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
 DE Gag-pro-pol fusion (Fragment).  
 OS Enzootic nasal tumour virus of goats.  
 OC Viruses; Retroviridae; Retroviridae; Betaretrovirus.  
 NCBI\_Taxid=239365;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22749839; PubMed=12867657;  
 RA Orlin A., Consens C., Minguillon E., Pascual Z., Villarreal M.P.,  
 RT "Characterization of enzootic nasal tumour virus of goats: complete  
 RT sequence and tissue distribution."  
 RL J. Gen. Virol. 84:2245-2252 (2003).  
 DR EMBL, AY197548; AAC05306.2; -.  
 FT NON TER 1  
 SQ SEQUENCE 870 AA; 99214 MW; 346D1642CDA4C3D4 CRC64;

Query Match  
 Best Local Similarity 71.9%; Score 46; DB 15; Length 870;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Dr 1 WYDPLTKLW 9  
 813 WKDPLTNLW 821

## RESULT 4

09S102 PRELIMINARY; PRT; 383 AA.  
 AC 09S102; PRELIMINARY; PRT; 383 AA.  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE At2g22030 protein (Hypothetical protein).  
 GN AT2g22030.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.  
 NCBI\_Taxid=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=20083487; PubMed=10617197;  
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,  
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,  
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,  
 RA Adams L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,  
 RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eissen J.A.,

RA Salzberg S.L., Fraser C.M., Venter J.C.;  
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis  
 RT thaliana."  
 RL Nature 402:761-768 (1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RA Lin X.;  
 RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

Dr 1 WYDPLTKLW 9  
 288 WYDPLTKLW 296

Query Match  
 Best Local Similarity 70.3%; Score 45; DB 10; Length 383;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Dr 1 WYDPLTKLW 9  
 288 WYDPLTKLW 296

## RESULT 5

09KA06 PRELIMINARY; PRT; 482 AA.  
 AC 09KA06; PRELIMINARY; PRT; 482 AA.  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Hypothetical protein BH2231.  
 GN BH2231.  
 OS Bacillus halodurans.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 NCBI\_Taxid=86665;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C-125 / JCM 9153;  
 RX MEDLINE=20512582; PubMed=11058132;  
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,  
 RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kihara S.,  
 RA Horikoshi K.;  
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus  
 RT halodurans and genomic sequence comparison with Bacillus subtilis."  
 RL Nucleic Acids Res. 28:4317-4331 (2000).  
 DR EMBL, AP001514; BAB05950.1; -.  
 DR PIR: G83928; G83928.  
 DR InterPro: IPR001173; Glyco\_trans\_2.  
 DR Pfam: PF00355; Glycoe\_transf\_2; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 482 AA; 54881 MW; CFI15B8CF8982AD CRC64;

Query Match  
 Best Local Similarity 70.3%; Score 45; DB 16; Length 482;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Dr 1 WYDPLTKLW 9  
 70 WKDPLTNLW 70



Db 443 WYRLTVLM 451

## RESULT 6

O9VGE6 PRELIMINARY; PRT; 538 AA.

AC O9VGE6; ID 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
 DE CG3571 protein.  
 GN CG3571.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NC NCB1\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley;  
 RX MEDLINE=20196006; PubMed=10731132.  
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Burton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fosler G., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalaal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kechum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kratz C., Kravitz S., Kulp D., Lai Z.,  
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kimms I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195 (2000).  
 DR EMBL; AB003694; AAF54738.1; -;  
 DR FLYBase; FBgn0037978; CG3571.  
 DR GO; GO:0005315; F:Protein binding; IEA.  
 DR InterPro; IPR000210; BTB\_POZ.  
 DR InterPro; IPR006652; Kelch\_rep.  
 DR Pfam; PF00651; BTB; 1.  
 DR Pfam; PF01344; Kelch; 6.  
 DR SMART; SM00225; BTB; 1.  
 DR SMART; SM00612; Kelch; 6.  
 DR PROSITE; PSS0097; BTB; 1.  
 SO SEQUENCE 538 AA; 60427 MW; 93675C9A5726EBBF CRC64;

Query Match 67.2%; Score 43; DB 5; Length 538;  
 Best Local Similarity 87.5%; Pred. No. 51;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

## OY 2 YDPLTKLM 9

Db 275 YDPLTKSM 282

## RESULT 7

O17698 PRELIMINARY; PRT; 570 AA.

AC O17698; ID 01-JAN-1998 (TREMblrel. 05, Created)  
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)  
 DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)  
 DE C53A5.6 protein.  
 GN C53A5.6.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peloderiinae; Caenorhabditis.  
 NC NCB1\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA Mortimore B.J.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 RP SEQUENCE FROM N.A.  
 RX none;  
 RA none;  
 RT "Genome sequence of the nematode C. elegans: A platform for  
 RT investigating biology.";  
 RL Science 282:2012-2018 (1998).  
 CC -1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL; Z81486; CAB03987.1; -;  
 DR PIR; T20166; T20166.  
 DR WormPep; C53A5.6; CE08955.  
 DR InterPro; IPR006651; Kelch.  
 DR InterPro; IPR006652; Kelch\_rep.  
 DR InterPro; IPR001841; Znf\_fing.  
 DR Pfam; PF01344; Kelch; 6.  
 DR Pfam; PF00097; Zf-C3HC4; 1.  
 DR PRINTS; PR00501; KELCHREPEAT.  
 DR SMART; SM00501; Kelch; 4.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PSS0089; ZF\_RING\_2; 1.  
 KW Metal-binding; Zinc; Zinc-finger.  
 SO SEQUENCE 570 AA; 63294 MW; 58B5E1BE24FBA0F5 CRC64;

Query Match 67.2%; Score 43; DB 5; Length 570;  
 Best Local Similarity 87.5%; Pred. No. 54;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

## OY 2 YDPLTKLM 9

Db 492 YDPLTKSM 499

## RESULT 8

O9VGE5 PRELIMINARY; PRT; 575 AA.

AC O9VGE5; ID 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
 DE CG3571 protein (LDA2169P).  
 GN CG3571.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NC NCB1\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley;

RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer V., Baxter E.G., Helt G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-U., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasly E.M.,  
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
 RA Bokorva D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,  
 RA Butris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Dou P.L., Downes M., Durbin K.J., Evans R., Fritze E.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
 RA Foaier C., Gabrielian A.B., Gary N.S., Gelbart W.M., Glasser K.,  
 RA Gocke A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,  
 RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Khamel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Matei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
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 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spindler A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter B., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,  
 RA Williams S.M., Woodage T., Wooley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao X., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195 (2000).  
 RN  
 RP  
 RC STRAIN=Berkley;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nuno J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,  
 RA Xu C., Lewis S.E., Rubin G.M., Celniker S.,  
 RL Submitted (Aug-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AEO03694; AAF54737.1; -;  
 DR EMBL; AY051950; AAK93374.1; -;  
 DR FLYBASE; FBgn0037978; CG3571.  
 DR GO; GO:0005515; P:protein binding; IEA.  
 DR InterPro; IPR000210; BTB\_PZ.  
 DR InterPro; IPR006552; Kelch\_rep.  
 DR Pfam; PF00651; BTB; 1.  
 DR Pfam; PF01344; Kelch; 6.  
 DR SMART; SMO0225; BTB; 1.  
 DR SMART; SMO0612; Kelch; 6.  
 DR PROSITE; PS0097; BTB; 1.  
 SQ SEQUENCE 575 AA; 6483 MW; 608F3BE4A6FA8283 CRC64;  
 Query Match 67.2%; Score 43; DB 5; Length 575;  
 Best Local Similarity 87.5%; Pred. No. 54;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 YDPLTKLM 9  
 Db 312 YDPLTKLM 319

AC Q85VAL; PRELIMINARY; PRT; 947 AA.  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 21, Last sequence update)  
 DE R010407p.  
 GN CG7097.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NX NCB1\_Taxid=7227;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E.,  
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,  
 RA Miranda A., Mungall C.J., Nuno J., Pacle J., Paragas V., Park S.,  
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celniker S.,  
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AY071688; AAL49310.1; -;  
 DR FLYBASE; FBgn0034421; CG7097.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0005083; F:small GTPase regulatory/interacting protein. . .; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR00180; Citeon.  
 DR InterPro; IPR00719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR Pfam; PF00780; CNH; 1.  
 DR Pfam; PF00069; pk\_nase; 1.  
 DR ProDom; PDD00001; Prot\_kinase; 1.  
 DR SMART; SMO0036; CNH; 1.  
 DR SMART; SMO0220; S\_TKC; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS0011; PROTEIN\_KINASE\_DOM; 1.  
 KW ATP-binding; Transferase.  
 SQ SEQUENCE 947 AA; 105224 MW; 814262CBD95FF56D CRC64;  
 Query Match 67.2%; Score 43; DB 5; Length 947;  
 Best Local Similarity 70.0%; Pred. No. 89;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 WYDPLTKML 10  
 Db 729 WYDPLTKML 738  
 RESULT 10  
 Q8ML18  
 ID Q8ML18 PRELIMINARY; PRT; 947 AA.  
 AC Q8ML18;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DE CG7097-PB.  
 GN CG7097.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NX NCB1\_Taxid=7227;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E.,  
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,  
 RA Miranda A., Mungall C.J., Nuno J., Pacle J., Paragas V., Park S.,  
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celniker S.,  
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AY071688; AAL49310.1; -;  
 DR FLYBASE; FBgn0034421; CG7097.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0005083; F:small GTPase regulatory/interacting protein. . .; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR00180; Citeon.  
 DR InterPro; IPR00719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR Pfam; PF00780; CNH; 1.  
 DR Pfam; PF00069; pk\_nase; 1.  
 DR ProDom; PDD00001; Prot\_kinase; 1.  
 DR SMART; SMO0036; CNH; 1.  
 DR SMART; SMO0220; S\_TKC; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS0011; PROTEIN\_KINASE\_DOM; 1.  
 KW ATP-binding; Transferase.  
 SQ SEQUENCE 947 AA; 105224 MW; 814262CBD95FF56D CRC64;  
 Query Match 67.2%; Score 43; DB 5; Length 947;  
 Best Local Similarity 70.0%; Pred. No. 89;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 WYDPLTKML 10  
 Db 729 WYDPLTKML 738

RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abill J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew K.Y., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Broctier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Duthin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris N.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Matvei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nussekern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svrtkase R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang X., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "the genome sequence of Drosophila melanogaster";  
 RL Science 287:2185-2195(2000).  
 [12]  
 RN SEQUENCE FROM N.A.  
 RP Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,  
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
 RA Barzon J., An H., Baldwin D., Barzon J., Beeson K.Y., Busam D.A.,  
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Drenek D., Farfan D.,  
 RA Ferletta S., Frise E., Galle R.F., Garg N.S., George R.A.,  
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
 RA Ibegwam C., Jalali M., Murthy B., Nelson C., Nelson K.A., Nunoo J.,  
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,  
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
 RA Stapleton M., Strong R., Svrtkase R., Tector C., Tyler D.,  
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,  
 RT "Sequencing of Drosophila melanogaster genome";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [13]  
 RN SEQUENCE FROM N.A.  
 RP Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.,  
 RA Hredceky P., Huang Y., Kaminker J.S., Prochkin S.E., Smith C.D.,  
 RA Tuoy J.L., Bergman C., Bernan B., Carlson J.W., Celniker S.E.,  
 RA Clump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
 RA Krommiller B., Marshall B., Milburn G., Richter J., Russo S.,  
 RA Searle S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,  
 RA Asburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,  
 RT "Annotation of Drosophila melanogaster genome";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [14]  
 RN SEQUENCE FROM N.A.  
 RP Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.,  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [15]  
 RP SEQUENCE FROM N.A.  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE003796; AAM70845.1; -  
 DR FLYBase; FBgn0034421; CG7097.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0005083; F:small GTPase regulatory/interacting protein. . .; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR001180; Citron.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR002290; Ser Thr kinase.  
 DR InterPro; IPR001245; Tyr kinase.  
 DR Pfam; PF00780; CNH; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR ProDom; PD000001; Prot kinase; 1.  
 DR SMART; SM00036; CNH; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR SMART; SM00219; TYK; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR ATP-binding; Transferase.  
 SQ SEQUENCE 947 AA; 105195 MW; 480EC8A8AE0D0E0 CRC64;  
 Query Match 67.2%; Score 43; DB 5; Length 947;  
 Best Local Similarity 70.0%; Pred. No. 89;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 WYDPLTKML 10  
 Db 729 WYDPLTKML 738  
 RESULT 11  
 Q9VBR6 PRELIMINARY; PRT; 1218 AA.  
 AC Q9VBR6  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE CG7097 protein.  
 GN CG7097  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abill J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew K.Y., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Broctier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Duthin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris N.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Matvei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nussekern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson W., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Swirskae R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang Q., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003766; AAF57595.1; -.  
 DR HSSP: O63450; 1A06.  
 DR FLYbase; FBgn0034421; CG7097.  
 DR GO: GO:0005524; F:ATP binding; IEA.  
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO: GO:0005083; F:small GTPase regulatory/interacting protein. . ; IEA.  
 DR GO: GO:0016740; F:transferase activity; IEA.  
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro: IPR001180; CItrom.  
 DR InterPro: IPR000719; Prot\_kinase.  
 DR Pfam: PF00780; CNH; 1.  
 DR Pfam: PF00069; pkinase; 1.  
 DR ProDom: PD000001; Prot\_kinase; 1.  
 DR SMART; SM00036; CNH; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR ATP-binding; Transferase  
 SQ SEQUENCE 1218 AA; 132395 MW; 7847F9F80CEDC8 CRC64;

Query Match 67.2%; Score 43; DB 5; Length 1218;  
 Best Local Similarity 70.0%; Pred. No. 1.1e+02;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 WYDPLTKLWL 10  
 Db 1000 WYDPLTKLWL 1009

RESULT 12  
 Q89RUI PRELIMINARY; PRT; 119 AA.  
 AC Q89RUI;  
 DT 01-JUN-2003 (TRENBLrel. 24, Created)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE BLR2671 protein.  
 GN BLR2671.  
 OS Bradyrhizobium japonicum.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Bradyrhizobiales; Bradyrhizobium.  
 OX NCBI\_TaxID=375;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=USDA 110;  
 RX MEDLINE=22484998; PubMed=12597275;  
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,  
 RA Sasamoto S., Watanabe A., Ideawa K., Itiguchi M., Kawashima K.,  
 RA Kohara M., Matsunoto M., Shimizu S., Tsunooka H., Wada T., Yamada M.,  
 RA Tabata S.;  
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium  
 RT Bradyrhizobium japonicum USDA110.";  
 RL DNA Res. 9:189-197(2002).  
 DR EMBL: AP005944; BAC47936.1; -.  
 DR Complete proteome.  
 SQ SEQUENCE 119 AA; 13303 MW; 799D98A891244914 CRC64;

Query Match 65.6%; Score 42; DB 16; Length 119;  
 Best Local Similarity 50.0%; Pred. No. 17;  
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10  
 Db 71 WYDPLTKLWL 80

RESULT 13  
 Q89RUI PRELIMINARY; PRT; 176 AA.  
 AC Q89RUI;  
 DT 01-JUN-2002 (TRENBLrel. 21, Created)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE Predicted protein.  
 GN MA2114.  
 OS Methanosarcina acetivorans.  
 OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;  
 OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.  
 OX NCBI\_TaxID=2214;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C2A / ATCC 35395 / DSM 2834;  
 RX MEDLINE=21929760; PubMed=11932238;  
 RA Galagan J.E., Nusbaum C., Koy A., Endrizzi M.G., MacDonald P.,  
 RA Fitzhugh W., Galvo S., Engels R., Smirnov S., Ancoor D., Brown A.,  
 RA Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R.,  
 RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,  
 RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guse A.M.,  
 RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,  
 RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,  
 RA Springer T.A., Umayahara L.A., White O., White R.H., de Macario E.C.,  
 RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,  
 RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,  
 RA Metcalf W.W., Birren B.;  
 RT "The genome of *Methanosarcina acetivorans* reveals extensive metabolic  
 RT and physiological diversity.";  
 RL Genome Res. 12:532-542(2002).  
 DR EMBL: AE010898; AAM05512.1; -.  
 DR InterPro: IPR007404; DUF457.  
 DR Pfam: PF04307; DUF457; 1.  
 KV Complete proteome.  
 SQ SEQUENCE 176 AA; 20158 MW; 6E257BDCA71F2027 CRC64;

Query Match 65.6%; Score 42; DB 17; Length 176;  
 Best Local Similarity 66.7%; Pred. No. 25;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 WYDPLTKLWL 9  
 Db 105 WYDPLTKLWL 113

RESULT 14  
 Q7VRS7 PRELIMINARY; PRT; 227 AA.  
 AC Q7VRS7;  
 DT 01-OCT-2003 (TRENBLrel. 25, Created)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Putative urease accessory protein P.  
 GN URRF OR BRL522.  
 OS Candidatus Blochmannia floridanus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.  
 OX NCBI\_TaxID=203907;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=22784745; PubMed=12886019;  
 RA Gil R., Silva F.J., Zientz E., Delmotte F., Gonzalez-Candela F.,  
 RA Latorre A., Rausell C., Kamerbeek J., Gadau J., Hoellhobler B.,  
 RA van Ham R.C.H.J., Gross R., Moya A.;  
 RT "The genome sequence of *Blochmannia floridanus*: comparative analysis  
 RT of reduced genomes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:9388-9393(2003).

DR EMBL: BX248586; CAD83208.1; -  
 Complete proteome.  
 SQ SEQUENCE 227 AA; 26407 MW; 0A1B45979F9BC1B0 CRC64;

Query Match 65.6%; Score 42; DB 16; Length 227;  
 Best Local Similarity 55.6%; Pred. No. 32;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 WYDPLTKLM 9  
 |||||  
 Db 116 WKDPTNLW 124

# RESULT 15

O9YNA2 PRELIMINARY; PRT; 290 AA.

AC O9YNA2: PRELIMINARY; PRT; 290 AA.  
 DT 01-MAY-1999 (TREMBlrel. 10, Created)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Reverse transcriptase (Fragment).  
 GN GAG-POL OR POL.  
 OS Sheep pulmonary adenomatosis virus (Jaagsiekte sheep retrovirus)  
 OS (JSRV).  
 OC Viruses; Retrovirus; Retroviridae; Betaretrovirus.  
 OX NCBI\_TaxID=11746;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=J57;  
 RX MEDLINE=99296727; PubMed=10366570;  
 RA Bai J., Bishop J.V., Carlson J.O., Demartini J.C.;  
 RT "Sequence comparison of JSRV with endogenous proviruses: envelope  
 RT receptor." and a novel ORF with similarity to a G-protein-coupled  
 RT receptor."  
 RL Virology 258:333-343(1999).  
 CC -1- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS  
 CC (BY SIMILARITY).  
 DR EMBL: Y18303; CA77117.1; -  
 DR GO: GO:0003677; F:DNA binding; IEA.  
 DR GO: GO:0004519; F:endonuclease activity; IEA.  
 DR GO: GO:0016787; F:hydrolyase activity; IEA.  
 DR GO: GO:0008907; F:integrase activity; IEA.  
 DR GO: GO:0003964; F:RNA-directed DNA polymerase activity; IEA.  
 DR GO: GO:0016740; F:transferase activity; IEA.  
 DR GO: GO:0008270; F:zinc ion binding; IEA.  
 DR GO: GO:0015074; P:DNA integration; IEA.  
 DR GO: GO:0006310; P:DNA recombination; IEA.  
 DR InterPro: IPR001037; Integrase\_C.  
 DR InterPro: IPR003308; Integrase\_Zn.  
 DR InterPro: IPR001584; Rve.  
 DR Pfam: PF00552; Integrase\_1.  
 DR Pfam: PF02022; Integrase\_Zn; 1.  
 DR Pfam: PF00665; Ive; 1.  
 KW Endonuclease; Hydrolyase; Nucleotidyltransferase; Polyprotein;  
 KW RNA-directed DNA polymerase; Transferase.  
 FT NON TER 1  
 SQ SEQUENCE 290 AA; 33190 MW; C33D2BD840222210 CRC64;

Query Match 65.6%; Score 42; DB 15; Length 290;  
 Best Local Similarity 66.7%; Pred. No. 41;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 WYDPLTKLM 9  
 |||||  
 Db 229 WKDPTNLW 237

# RESULT 16

O9YNA2 PRELIMINARY; PRT; 291 AA.

AC O9YNA2: PRELIMINARY; PRT; 291 AA.  
 DT 01-MAY-1999 (TREMBlrel. 10, Created)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Reverse transcriptase (Fragment).  
 GN GAG-POL OR POL.  
 OS Sheep pulmonary adenomatosis virus (Jaagsiekte sheep retrovirus)  
 OS (JSRV).  
 OC Viruses; Retrovirus; Retroviridae; Betaretrovirus.  
 OX NCBI\_TaxID=11746;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=83RS28;  
 RX MEDLINE=99296727; PubMed=10366570;  
 RA Bai J., Bishop J.V., Carlson J.O., Demartini J.C.;  
 RT "Sequence comparison of JSRV with endogenous proviruses: envelope  
 RT receptor." and a novel ORF with similarity to a G-protein-coupled  
 RT receptor."  
 RL Virology 258:333-343(1999).  
 CC -1- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS  
 CC (BY SIMILARITY).  
 DR EMBL: Y18303; CA77117.1; -  
 DR GO: GO:0003677; F:DNA binding; IEA.  
 DR GO: GO:0004519; F:endonuclease activity; IEA.  
 DR GO: GO:0016787; F:hydrolyase activity; IEA.  
 DR GO: GO:0008907; F:integrase activity; IEA.  
 DR GO: GO:0003964; F:RNA-directed DNA polymerase activity; IEA.  
 DR GO: GO:0016740; F:transferase activity; IEA.  
 DR GO: GO:0008270; F:zinc ion binding; IEA.  
 DR GO: GO:0015074; P:DNA integration; IEA.  
 DR GO: GO:0006310; P:DNA recombination; IEA.  
 DR InterPro: IPR001037; Integrase\_C.  
 DR InterPro: IPR003308; Integrase\_Zn.  
 DR InterPro: IPR001584; Rve.  
 DR Pfam: PF00552; Integrase\_1.  
 DR Pfam: PF02022; Integrase\_Zn; 1.  
 DR Pfam: PF00665; Ive; 1.  
 KW Endonuclease; Hydrolyase; Nucleotidyltransferase; Polyprotein;  
 KW RNA-directed DNA polymerase; Transferase.  
 FT NON TER 1  
 SQ SEQUENCE 291 AA; 33372 MW; 34912961BDEE4FB CRC64;

Query Match 65.6%; Score 42; DB 15; Length 291;  
 Best Local Similarity 66.7%; Pred. No. 41;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 WYDPLTKLM 9  
 |||||  
 Db 230 WKDPTNLW 238

# RESULT 17

O49488 PRELIMINARY; PRT; 293 AA.

AC O49488: PRELIMINARY; PRT; 293 AA.  
 DT 01-JUN-1998 (TREMBlrel. 06, Created)  
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN F28A23.70 OR ATG34170.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eustoids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bevan M., Weichselgartner M., Fartmann B., Grandérath K., Dauner D.,  
 RA Herzl A., Neumann S., Hobeisel J., Jesse T., Heijnen L., Vos P.,  
 RA Mewes H.W., Mayer K., Scheller C.;  
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Weichselgartner M., Fartmann B., Grandérath K., Dauner D., Herzl A.,  
 RA Neumann S., Mewes H.W., Lemcke K., Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

```

RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL021961; CAA17555.1; -
DR EMBL; AL161585; CAB80134.1; -
DR PIR; T05419; T05419.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR006652; Kelch_rep.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF0344; Kelch; 2.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00612; Kelch; 2.
KW Hypothetical protein.
SQ SEQUENCE 293 AA; 33448 MW; 5049260E168800E CRC64;

Query Match 65.6%; Score 42; DB 10; Length 293;
Best Local Similarity 55.6%; Pred. No. 41;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Cy 1 WYDPLTKLM 9
Db 244 WYDPERRW 252

RESULT 18
ID 081798 PRELIMINARY; PRT; 374 AA.
AC 081798;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Putative polygalacturonase (Fragment).
GN P8D20.180 OR AT4G35670.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Koester P., Hempel S., Entian K.-D., Honeisel J., Jesse T.,
RA Heinen L., Vos P., Mewes H.W., Mayer K.F.X., Scheller C., Bevan M.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES
CC (POLYGLACTURONASES).
DR EMBL; AL031135; CAA20037.1; -
DR EMBL; AL161587; CAB80283.1; -
DR PIR; B85421; B85421.
DR PIR; T04672; T04672.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0004650; F:polygalacturonase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR000743; Glyco_hydro_28.
DR InterPro; IPR006626; Pbh1.
DR Pfam; PF00295; Glyco_hydro_28; 1.
DR SMART; SM00710; Pbh1; 5.
DR PROSITE; PS00502; POLYGLACTURONASE; 1.
KW Cell wall; Glycosidase; Hydrolase; Signal.
FT NON TER 1
SQ SEQUENCE 374 AA; 39884 MW; 3B86DB19DFB1ACB9 CRC64;

Query Match 65.6%; Score 42; DB 10; Length 374;
Best Local Similarity 40.0%; Pred. No. 52;

Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Cy 1 WYDPLTKLM 10
Db 91 WSDPISRWMT 100

RESULT 19
ID 095VA3 PRELIMINARY; PRT; 392 AA.
AC 095VA3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein (At4G39550).
GN F23K16.180 OR AT4G39550.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
RA Mayer K.F.X., Lemcke K., Scheller C.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Murphy G., Ridley P., Hudson S., Mewes H.W., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Shun P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P.,
RA Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hewan V.W.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL078620; CAB44690.1; -
DR EMBL; AL161595; CAB80618.1; -
DR EMBL; BT003146; AAC24578.1; -
DR PIR; T09371; T09371.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR006652; Kelch_rep.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF0344; Kelch; 2.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00612; Kelch; 2.
KW Hypothetical protein.
SQ SEQUENCE 392 AA; 44269 MW; 1EE507551D61FB7B CRC64;

Query Match 65.6%; Score 42; DB 10; Length 392;
Best Local Similarity 55.6%; Pred. No. 55;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Cy 1 WYDPLTKLM 9
Db 297 WYDTMARLM 305

RESULT 20
Q91HT7

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ID Q91H17 PRELIMINARY; PRT; 442 AA.  
AC Q91H17: 01-DEC-2001 (TREMblrel. 19, Created)  
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE Capsid protein.  
OS Discula destructiva virus 2.  
OC Viruses: dsRNA viruses; Partitiviridae; Partitiviruses.  
NCBI\_TaxID=160484;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=331;  
RA Rong R., Scott S.W., Rao S., Garner G.R., Tainter F.H.;  
RT "Cloning and sequencing of dsRNAs of a previously unreported virus  
found in Discula destructiva";  
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY033437; AAK59380.1; -  
SQ SEQUENCE 442 AA; 47916 MW; 81A5405361AB6979 CRC64;

Query Match 65.6%; Score 42; DB 12; Length 442;  
Best Local Similarity 60.0%; Pred. No. 62;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YDPLTKLM 10  
Db 212 WKPEPLRLML 221

RESULT 21  
Q9Y480 PRELIMINARY; PRT; 619 AA.  
AC Q9Y480:  
DT 01-NOV-1999 (TREMblrel. 12, Created)  
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)  
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
DE NS1-binding protein.  
GN NS1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98362120; PubMed=9696811;  
RA Wolff T., O'Neill R.B., Palese P.;  
RT "NS1-binding protein (NS1-BP): a novel human protein that interacts  
with the influenza A virus nonstructural NS1 protein is relocalized in  
the nuclei of infected cells";  
RL J. Virol. 72:7170-7180(1998).  
DR EMBL; AJ012449; CAI10029.1; -  
DR HSSP; Q05516; ICS3.  
DR GO; GO:0005515; F:protein binding; IEA.  
DR InterPro; IPR000210; BTB\_POZ.  
DR InterPro; IPR006651; Kelch.  
DR InterPro; IPR006652; Kelch\_rep.  
DR Pfam; PF00651; BTB; 1.  
DR Pfam; PF01344; Kelch; 6.  
DR PRINTS; PR00501; KELCHREPEAT.  
DR SMART; SM00225; BTB; 1.  
DR SMART; SM00612; Kelch; 5.  
DR PROSITE; PS50097; BTB; 1.  
SQ SEQUENCE 619 AA; 69032 MW; 5CFF8F5F2735DBA CRC64;

Query Match 65.6%; Score 42; DB 4; Length 619;  
Best Local Similarity 75.0%; Pred. No. 86;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YDPLTKLM 9  
Db 485 FDPVTKLM 492

RESULT 22

Q9NZX0 PRELIMINARY; PRT; 641 AA.  
AC Q9NZX0:  
DT 01-OCT-2000 (TREMblrel. 15, Created)  
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
DE HSPC068.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=20493367; PubMed=11042152;  
RA Zhang Q.H., Ye M., Wu X.Y., Ren S.X., Zhao M., Zhao C.J., Fu G.,  
RA Shen Y., Fan H.Y., Lu G., Zhong M., Xu X.R., Han Z.G., Zhang J.W.,  
RA Tao J., Huang Q.H., Zhou J., Hu G.X., Gu J., Chen S.J., Chen Z.;  
RT "Cloning and functional analysis of cDNAs with open reading frames for  
300 previously undefined genes expressed in CD34+ hematopoietic  
stem/progenitor cells";  
RL Genome Res. 10:1546-1560(2000).  
DR EMBL; AF161553; AAF29040.1; -  
DR HSSP; Q05516; ICS3.  
DR GO; GO:0005515; F:protein binding; IEA.  
DR InterPro; IPR000210; BTB\_POZ.  
DR InterPro; IPR006651; Kelch.  
DR InterPro; IPR006652; Kelch\_rep.  
DR Pfam; PF00651; BTB; 1.  
DR Pfam; PF01344; Kelch; 6.  
DR PRINTS; PR00501; KELCHREPEAT.  
DR SMART; SM00225; BTB; 1.  
DR SMART; SM00612; Kelch; 5.  
DR PROSITE; PS50097; BTB; 1.  
SQ SEQUENCE 641 AA; 71605 MW; B7451584FC79C87A CRC64;

Query Match 65.6%; Score 42; DB 4; Length 641;  
Best Local Similarity 75.0%; Pred. No. 89;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YDPLTKLM 9  
Db 484 FDPVTKLM 491

RESULT 23  
Q9Y6Y0 PRELIMINARY; PRT; 642 AA.  
AC Q9Y6Y0:  
DT 01-NOV-1999 (TREMblrel. 12, Created)  
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)  
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
DE Hypothetical protein KIAA0850 (NS1-binding protein-like protein).  
GN KIAA0850.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=99156230; PubMed=10048485;  
RA Miyagase T., Ishikawa K., Suyama M., Kikuno R., Hirogawa M.,  
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. XII.  
The complete sequences of 100 new cDNA clones from brain which code  
for large proteins in vitro";  
RL DNA Res. 5:355-364(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Chen B.S., Zhang K.M.;  
RT "A novel gene from endothelium cells stimulated by human plasma  
LDL-similar to NS1-binding protein.";

RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AR020657; BAA74873.1; -  
DR EMBL: AF205218; AAG43485.1; -  
DR HSP; Q05516; ICS3.  
DR GeneW; HGNC:16951; IVNS1ABP.  
DR GO; GO:0005681; Cisplatin complex; TMS.  
DR GO; GO:0005667; C:transcription factor complex; TMS.  
DR GO; GO:0006371; P:RNA splicing; TMS.  
DR GO; GO:0006315; P:response to viruses; TMS.  
DR InterPro; IPR00210; BTB\_POZ.  
DR InterPro; IPR006651; Kelch.  
DR InterPro; IPR006652; Kelch\_rep.  
DR Pfam; PF00651; BTB; 1.  
DR Pfam; PF01344; Kelch; 6.  
DR PRINTS; PRO0501; KELCHREPEAT.  
DR SMART; SM00225; BTB; 1.  
DR SMART; SM00612; Kelch; 5.  
DR PROSITE; PS0097; BTB; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 642 AA; 71729 MW; 456B30DC4E351CCD CRC64;  
  
Query Match 65.6%; Score 42; DB 4; Length 642;  
Best Local Similarity 75.0%; Pred. No. 89;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 YDPLTKLM 9  
Db 485 FDPVTKLM 492  
  
RESULT 24  
ID Q95N66 PRELIMINARY; PRT; 873 AA.  
AC Q95N66;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Polymerase (Fragment).  
GN POL.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21184705; PubMed=11287573;  
RA DeMartini J.C., Bishop J.V., Allen T.E., Jassim F.A., Sharp J.M.,  
de las Heras M., Voelker D.R., Carlson J.O.,  
"Jaagsiekte Sheep Retrovirus Proviral Clone JSRV(JS7), Derived from  
RT the JS7 Lung Tumor Cell Line, Induces Ovine Pulmonary Carcinoma and Is  
RT Integrated into the Surfactant Protein A Gene.",  
RL J. Virol. 75:4239-4246(2001).  
DR EMBL: AF357971; AAK38686.1; -  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0008907; F:integrase activity; IEA.  
DR GO; GO:0004523; F:ribonuclease H activity; IEA.  
DR GO; GO:0003723; F:RNA binding; IEA.  
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0008270; F:zinc ion binding; IEA.  
DR GO; GO:0015074; F:DNA integration; IEA.  
DR GO; GO:0006310; P:DNA recombination; IEA.  
DR GO; GO:0006278; P:RNA dependent DNA replication; IEA.  
DR InterPro; IPR001037; Integrase\_C.  
DR InterPro; IPR003308; Integrase\_Zn.  
DR InterPro; IPR001584; Rve.  
DR InterPro; IPR000477; RVTse.  
DR Pfam; PF00552; Integrase; 1.  
DR Pfam; PF02022; Integrase\_Zn; 1.  
DR Pfam; PF00075; rnaesh; 1.  
KW Non TER

DR Pfam; PF00665; rve; 1.  
DR Pfam; PF00078; rvt; 1.  
KW RNA-directed DNA polymerase; Transferase.  
FT NON TER  
SQ SEQUENCE 873 AA; 99548 MW; F7E218048661A541 CRC64;  
  
Query Match 65.6%; Score 42; DB 6; Length 873;  
Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 WYDPLTKLM 9  
Db 812 WKDPTNLM 820  
  
RESULT 25  
ID Q9WR73 PRELIMINARY; PRT; 874 AA.  
AC Q9WR73;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Pol (Fragment).  
GN GAG-POL OR POL.  
OS Sheep pulmonary adenomatosis virus (Jaagsiekte sheep retrovirus)  
OS (JSRV).  
OC Viruses; Retroviridae; Retroviridae; Betaretrovirus.  
OC NCBI\_TaxID=11746;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99329222; PubMed=10400795;  
RA Palmarini M., Sharp J.M., de las Heras M., Fan H.,  
RT "Jaagsiekte sheep retrovirus is necessary and sufficient to induce a  
RT contagious lung cancer in sheep."  
RL J. Virol. 73:6964-6972(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=JSRV21;  
RA Palmarini M., Sharp J.M., Fan H.,  
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- PPM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS  
CC (BY SIMILARITY).  
DR EMBL: AF105220; AAD45226.1; -  
DR HSP; P03355; 1MML.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0004519; F:endonuclease activity; IEA.  
DR GO; GO:0016787; F:hydrolyase activity; IEA.  
DR GO; GO:0008907; F:integrase activity; IEA.  
DR GO; GO:0004523; F:RNA binding; IEA.  
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0008270; F:zinc ion binding; IEA.  
DR GO; GO:0015074; P:DNA integration; IEA.  
DR GO; GO:0006310; P:DNA recombination; IEA.  
DR GO; GO:0006278; P:RNA dependent DNA replication; IEA.  
DR InterPro; IPR001037; Integrase\_C.  
DR InterPro; IPR003308; Integrase\_Zn.  
DR InterPro; IPR002156; Rnaesh.  
DR InterPro; IPR001584; Rve.  
DR InterPro; IPR000477; RVTse.  
DR Pfam; PF00552; Integrase; 1.  
DR Pfam; PF02022; Integrase\_Zn; 1.  
DR Pfam; PF00075; rnaesh; 1.  
DR Pfam; PF00665; rve; 1.  
DR Pfam; PF00078; rvt; 1.  
KW Endonuclease; Hydrolyase; Nucleotidyltransferase; Polyprotein;  
KW RNA-directed DNA polymerase; Transferase.  
FT NON TER  
SQ SEQUENCE 874 AA; 99701 MW; 85AC1ADE4DB97DB8 CRC64;  
  
Query Match 65.6%; Score 42; DB 15; Length 874;



Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLW 9  
Db 813 WYDPLTKLW 821

## RESULT 26

Q9AYF3 PRELIMINARY; PRT; 312 AA.  
AC Q9AYF3;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Putative protein.  
GN OSUNBA009409.17.  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhacroidae; Oryzae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA See L.H., Spiegel L.A., Nascimento L.U., de la Bastide M.,  
RA Preston R.R., Huang E.N., Rodriguez M.A., Vil M.D., Baker J.P.,  
RA Bahret A., Shah R.S., Miller B., Kirchoff K.A., King L., Toth K.,  
RA O'Shaughnessy A., Dedhia N.N., McCombie W.R.;  
RT "Genomic Sequence for Oryza sativa, Nipponbare strain, Chromosome X,  
RT Clone OSUNBA009409, complete sequence."  
RN Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.  
RL [2]  
RP SEQUENCE FROM N.A.  
RA McCombie W.R.;  
RN Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.  
RL [3]  
RP SEQUENCE FROM N.A.  
RA McCombie W.R.;  
RN Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.  
RL [4]  
RP SEQUENCE FROM N.A.  
RA Bal H.P., See L.H., Spiegel L.A., Nascimento L.U., de la Bastide M.,  
RA Preston R.R., Huang E.N., Rodriguez M.A., Vil M.D., Baker J.P.,  
RA Bahret A., Shah R.S., Miller B., Kirchoff K.A., King L., Toth K.,  
RA O'Shaughnessy A., Dedhia N.N., McCombie W.R.;  
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AC078839; AK13101.1; -.  
DR Gramene; Q9AYF3; -.  
DR InterPro; IPR006652; Kelch\_rep.  
DR Pfam; PF01344; Kelch; 3  
DR SMART; SM00612; Kelch; 3  
SQ SEQUENCE 312 AA; 34374 MW; 58818D5F80A7EBF CRC64;

Query Match 64.8%; Score 41.5; DB 10; Length 312;  
Best Local Similarity 63.6%; Pred. No. 53;  
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 WYDPLTKLW 10  
Db 97 WYDPLTKLW 107

## RESULT 27

Q7XF24 PRELIMINARY; PRT; 312 AA.  
AC Q7XF24;  
DT 01-OCT-2003 (TREMBlrel. 25, Created)  
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Hypothetical protein.  
GN OSUNBA009409.17.  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhacroidae; Oryzae; Oryza.  
OX NCBI\_TaxID=35947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=cv. Nipponbare;  
RA The Rice Chromosome 10 Sequencing Consortium;  
RT "in-depth view of structure, activity, and evolution of rice  
RT chromosome 10."  
RN Science 300:1566-1569 (2003).  
RL [2]  
RP SEQUENCE FROM N.A.  
RA STRAIN=cv. Nipponbare;  
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;  
RL Submitted (MAY-2003) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AE017089; AAP3535.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 312 AA; 34374 MW; 58818D5F80A7EBF CRC64;

Query Match 64.8%; Score 41.5; DB 10; Length 312;  
Best Local Similarity 63.6%; Pred. No. 53;  
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 WYDPLTKLW 10  
Db 97 WYDPLTKLW 107

## RESULT 28

Q9R728 PRELIMINARY; PRT; 144 AA.  
AC Q9R728;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Z12F protein.  
GN Z12F.  
OS Vibrio cholerae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrio.  
OX NCBI\_TaxID=666;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=Z17561;  
RA Fallarino A.;  
RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AJ231083; CA13125.1; -.  
DR InterPro; IPR000160; GGDEF.  
DR Pfam; PF00990; GGDEF; 1.  
DR PROSITE; PS50887; GGDEF; 1.  
SQ SEQUENCE 144 AA; 17072 MW; 802739ADB8A823D5A CRC64;

Query Match 64.1%; Score 41; DB 2; Length 144;  
Best Local Similarity 75.0%; Pred. No. 30;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLW 8  
Db 91 WHDPLTKLW 98

## RESULT 29

O87030 PRELIMINARY; PRT; 168 AA.  
AC O87030;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Z13F protein (Fragment).  
GN Z13F.  
OS Vibrio cholerae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrio.

```

OX NCBI_Taxid=666;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=217561;
RA Fallarino A.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ231085; CA13127.1; -
DR InterPro; IPR000160; GDEP.
DR Pfam; PF00990; GDEP.1.
DR PROSITE; PS50867; GDEP.1.
FT NON_TER
RN
SQ SEQUENCE 168 AA; 19864 MW; A2A14C6C76388FBD CRC64;

Query Match
Best Local Similarity 64.1%; Score 41; DB 2; Length 168;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKL 8
DB 115 WHDPLTRL 122

RESULT 30
Q88XC1 PRELIMINARY; PRT; 309 AA.
AC Q88XC1;
DT 01-JUN-2003 (TREMblrel. 24, Created)
DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
DE 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Homocysteine S-methyltransferase (EC 2.1.1.10).
GN LP_1298.
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_Taxid=1590;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=NCIMB 8826 / WCF51;
RX MEDLINE=22480296; PubMed=1256566;
RA Klebebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
RA De Vos W.M., Stezen R.U.;
RT "Complete genome sequence of Lactobacillus plantarum WCF51.";
RT Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
DR EMBL; AL935255; CAD63793.1; -
DR GO; GO:0008898; F:homocysteine S-methyltransferase activity; IEA.
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR003726; S_methyl_trans.
DR Pfam; PF02574; S-methyl_trans.
DR Methyltransferase; Transferase; Complete proteome.
SQ SEQUENCE 309 AA; 32891 MW; B0C8592D25C1333 CRC64;

Query Match
Best Local Similarity 64.1%; Score 41; DB 16; Length 309;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YDPLTKLW 9
DB 252 YDPLTKW 259

RESULT 31
Q8VWL8 PRELIMINARY; PRT; 514 AA.
AC Q8VWL8;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Beta-mannosidase (beta-mannosidase enzyme).
DR Lycopersicon esculentum (Tomato).

OX Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Solanum.
OX NCBI_Taxid=4081;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=cv. glamour;
RA Mo B., Bewley J.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Glamour; TISSUE=Seed;
RA Mo B., Bewley J.;
RT "Lycopersicon esculentum beta-mannosidase (Lewside) gene encoding
RT beta-mannosidase enzyme, complete sequence.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF413204; AL37719.1; -
DR EMBL; AF403444; AL37714.1; -
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001360; Glyco_hydro_1.
DR Pfam; PF00232; Glyco_hydro_1.
DR PRINTS; PR00131; GLYDRIASE1.
DR Prodom; PD000650; Glyco_hydro_1.
DR PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; 1.
SQ SEQUENCE 514 AA; 59288 MW; 0A3859084EDA1971 CRC64;

Query Match
Best Local Similarity 64.1%; Score 41; DB 10; Length 514;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTK 7
DB 281 WYDPLTK 287

RESULT 32
Q81V89 PRELIMINARY; PRT; 539 AA.
AC Q81V89;
DT 01-JUN-2003 (TREMblrel. 24, Created)
DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE L-lactate permease.
GN LLDP-1 OR BA0610.
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_Taxid=198094;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=22608414; PubMed=12721629;
RA Neid T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Riddlestone J., Wu M.,
RA Kolonay J.F., Beaman M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy S.C., Madhu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Kadane D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plant R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salberg S.L.,
RA Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RT Nature 423:81-86(2003).
DR EMBL; AE017026; AAP24628.1; -
DR TIGR; BA0610; -
DR GO; GO:0015129; F:lactate transporter activity; IEA.
DR GO; GO:0015727; P:lactate transport; IEA.
DR InterPro; IPR003804; Lactate_perm.
DR Pfam; PF02652; Lactate_perm.1.
DR TIGRPFAM; TIGR00795; lctP; 1.
```

KW Complete proteome. 539 AA; 57559 MW; 6018C32DA39DCEA3 CRC64;  
 SQ SEQUENCE 539 AA; 57559 MW; 6018C32DA39DCEA3 CRC64;  
 Query Match 64.1%; Score 41; DB 16; Length 539;  
 Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 YDPLTKLWL 10  
 |||||:  
 8 YDPLNNIWL 16

DB

RESULT 33  
 081113 PRELIMINARY; PRT; 539 AA.  
 AC 081113;  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE L-lactate permease.  
 GN BC0612.  
 OS Bacillus cereus (strain ATCC 14579 / DSM 31).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=226900;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22608415; PubMed=12721630;  
 RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candolon B.,  
 RA Kaparell V., Bhattacharya A., Resnik G., Mikhailova N., Lapidus A.,  
 RA Chu L., Mazur M., Goldsman E., Larsen N., D'Souza M., Malunas T.,  
 RA Grechkin Y., Pusch G., Haselkorn R., Fomstein M., Ehrlich S.D.,  
 RA Overbeek R., Kyrpides N.,  
 RT "Genome sequence of Bacillus cereus and comparative analysis with  
 RT Bacillus anthracis."  
 RL Nature 423:87-91(2003).  
 DR EMBL; AE016999; AAP07630.1;  
 DR GO; GO:0015129; P.lactate transporter activity; IEA.  
 DR GO; GO:0015727; P.lactate transport; IEA.  
 DR InterPro; IPR003804; Lactate\_perm.  
 DR Pfam; PF02652; Lactate\_perm.  
 DR Trifam; TIGR00795; lctP; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 539 AA; 57523 MW; E3891C8E9CD48ABA CRC64;

OY 2 YDPLTKLWL 10  
 |||||:  
 8 YDPLNNIWL 16

DB

RESULT 34  
 07VIF7 PRELIMINARY; PRT; 591 AA.  
 AC 07VIF7;  
 DT 01-OCT-2003 (TREMBlrel. 25, Created)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE L-lactate permease (EC 2.7.1.69).  
 GN LDDP OR H00649.  
 OS Helicobacter hepaticus.  
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
 OC Helicobacteraceae; Helicobacter.  
 OX NCBI\_TaxID=32025;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=ATCC 51449 / 3B1;  
 MEDLINE=22709201; PubMed=12810954;  
 RA Stuerbaum S., Josephans C., Stezenbach T., Dreescher B., Brandt P.,  
 RA Bell M., Droege M., Farman B., Fischer H.-P., Ge Z., Hoerster A.,  
 RA Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G.,

RA Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.;  
 RT "The complete genome sequence of the carcinogenic bacterium  
 RT Helicobacter hepaticus."  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906 (2003).  
 DR EMBL; AE017146; AAP77246.1;  
 KW Transferrase; Complete proteome.  
 SQ SEQUENCE 591 AA; 63491 MW; BCE79F374AA462DA CRC64;

OY 2 YDPLTKLWL 10  
 |||||:  
 8 YDPLNNIWL 16

DB

RESULT 35  
 08A125 PRELIMINARY; PRT; 604 AA.  
 AC 08A125;  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Beta-galactosidase.  
 GN BT3513.  
 OS Bacteroides thetaiotaomicron.  
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
 OC Bacteroidaceae; Bacteroides.  
 OX NCBI\_TaxID=818;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=VPI-5482 / ATCC 29148;  
 MEDLINE=22550858; PubMed=12663928;  
 RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,  
 RA Chang H.C., Hooper L.V., Gordon J.I.;  
 RT "A genomic view of the human Bacteroides thetaiotaomicron symbiosis."  
 RL Science 299:2074-2076(2003).  
 DR EMBL; AE016940; AA078619.1;  
 DR GO; GO:0044553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR008979; Gal\_bind\_like.  
 DR InterPro; IPR006102; Glyco\_hydro\_21g.  
 DR InterPro; IPR006104; Glyco\_hydro\_25g.  
 DR InterPro; IPR04792; HI0933\_like.  
 DR Pfam; PF00703; Glyco\_hydro\_2; 1.  
 DR Pfam; PF02837; Glyco\_hydro\_2 N; 1.  
 DR ProDom; PD018041; HI0933\_like; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 604 AA; 68822 MW; 75E369E21AC683AD CRC64;

OY 1 WYDPLTKLWL 9  
 |||||:  
 193 WYTPVTGIW 201

DB

RESULT 36  
 09K0R4 PRELIMINARY; PRT; 655 AA.  
 AC 09K0R4;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE GGBP family protein.  
 GN VCI1934.  
 OS Vibrio cholerae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrio.  
 OX NCBI\_TaxID=666;

[1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=BI Tor N16961 / Serotype O1;  
 RX MEDLINE=20406833; PubMed=10952301;  
 RA Heideberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,  
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayan L.A.,  
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,  
 RA Ermolaeva M.D., Vamathevan J., Bass S., Olin H., Dragoi I., Sellers P.,  
 RA McDonald L., Ueberback T., Fleischmann R.D., Nierman W.C., White O.,  
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,  
 RA Fraser C.M.;  
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio  
 RT cholerae.";  
 RL Nature 406:477-483(2000).  
 DR EMBL; AE004269; AAF95082.1; -  
 DR PIR; P82138; P82138.  
 DR TIGR; VCI1934; -  
 DR InterPro; IPR001633; EAL.  
 DR InterPro; IPR00160; GGDEF.  
 DR Pfam; PF00563; EAL; 1.  
 DR Pfam; PF00990; GGDEF; 1.  
 DR SMART; SM00267; DUF1; 1.  
 DR SMART; SM00552; DUF2; 1.  
 DR TIGRFAMs; TIGR00254; GGDEF; 1.  
 DR PROSITE; PS00883; EAL; 1.  
 DR PROSITE; PS00887; GGDEF; 1.  
 DR Complete proteome.  
 KW SEQUENCE 655 AA; 76008 MW; 5B6F30F3904D348 CRC64;  
 SQ  
 Query Match 64.1%; Score 41; DB 16; Length 655;  
 Best Local Similarity 75.0%; Pred. No. 1.3e+02;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 WYDPLTKL 8  
 Db 213 WYDPLTKL 220  
 RESULT 37  
 ID 0910K3 PRELIMINARY; PRT; 672 AA.  
 AC 0910K3;  
 DT 01-MAR-2001 (TRENBLrel. 16, Created)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Hypothetical protein PA2635.  
 GN PA2635.  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 15692 / PA01;  
 RX MEDLINE=20437337; PubMed=10984043;  
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,  
 RA Hickey M.D., Brinkman F.S.L., Hutmagle W.O., Kowalik D.J., Lagrou M.,  
 RA Gatter R.L., Goltz L., Tolentino E., Westbrock-Wadman S., Yuan Y.,  
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Laidig K., Lim R.M.,  
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Mu Z., Paulsen I.T.,  
 RA Reizer J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.;  
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
 RT opportunistic pathogen.";  
 RL Nature 406:959-964(2000).  
 DR EMBL; AE004692; AAC06023.1; -  
 DR PIR; H83315; H83315.  
 DR InterPro; IPR008557; DUF839.  
 DR InterPro; IPR006311; Tat.  
 DR Pfam; PF05787; DUF839; 1.  
 DR TIGRFAMs; TIGR01409; TAT\_signal\_seq; 1.  
 DR Hypothetical protein; Complete proteome.  
 KW SEQUENCE 672 AA; 73886 MW; 364AB67B411CFC80 CRC64;  
 SQ

Query Match 64.1%; Score 41; DB 16; Length 672;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 WYDPLTKL 10  
 Db 566 WYDPLTKL 575  
 RESULT 38  
 ID 08L1Z1 PRELIMINARY; PRT; 694 AA.  
 AC 08L1Z1;  
 DT 01-OCT-2002 (TRENBLrel. 22, Created)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Exonuclease V alpha subunit RecD.  
 GN RECD.  
 OS Pseudomonas syringae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=317;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Begha K., Ray M.K.;  
 RT "recD gene is essential for growth at low temperature in the Antarctic  
 RT psychrotrophic bacterium Pseudomonas syringae.";  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY078390; AAL79573.1; -  
 DR GO; GO:0009338; C:exodeoxyribonuclease V complex; IEA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0008854; F:exodeoxyribonuclease V activity; IEA.  
 DR GO; GO:0000166; F:nucleotide binding; IEA.  
 DR InterPro; IPR003593; AAA\_ATPase.  
 DR InterPro; IPR000585; Hemopexin.  
 DR InterPro; IPR006344; RecD.  
 DR SMART; SM00382; AAA; 1.  
 DR TIGRFAMs; TIGR01447; RECD; 1.  
 DR PROSITE; PS00024; HEMOPEXIN; 1.  
 DR ATP-binding.  
 KW SEQUENCE 694 AA; 76075 MW; FF4D48115D47B10C CRC64;  
 SQ  
 Query Match 64.1%; Score 41; DB 2; Length 694;  
 Best Local Similarity 60.0%; Pred. No. 1.4e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 WYDPLTKL 10  
 Db 375 WYDPLTKL 384  
 RESULT 39  
 ID 07UUT4 PRELIMINARY; PRT; 733 AA.  
 AC 07UUT4;  
 DT 01-OCT-2003 (TRENBLrel. 25, Created)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN RBL105.  
 OS Rhodospirillum rubrum.  
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;  
 OC Planctomycetaceae; Pirellula.  
 OX NCBI\_TaxID=117;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1;  
 RX MEDLINE=22735913; PubMed=12835416;  
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,  
 RA Ludwig W., Gade D., Beck A., Borzym K., Heilmann K., Rabus R.,  
 RA Schleiner H., Amann R., Reinhardt K.;  
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.  
 RT strain 1.";

RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).  
 DR EMBL: BX294152; CAD7137.1; -  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 733 AA; 81016 MW; 4432EA709BBF62E CRC64;

Query Match 64.1%; Score 41; DB 16; Length 733;  
 Best Local Similarity 70.0%; Pred. No. 1.5e+02;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WDPLTKLWL 10  
 DB 451 WDPNGKLWL 460

RESULT 40

070021 PRELIMINARY; PRT; 808 AA.  
 AC 070021;  
 DT 01-AUG-1998 (TREMBLrel. 07, Created)  
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Beta-glucosidase.  
 GN ERYBI.  
 OS Saccharopolyspora erythraea (Streptomyces erythraeus).  
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;  
 OC Pseudonocardiales; Pseudonocardaceae; Saccharopolyspora.  
 CX NCBI\_TaxId=1836;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRRL2338;  
 RX MEDLINE=98273631; PubMed=9613575;  
 RA Gaisner S., Boehm G.A., Douthett M., Raynal M.C., Dillon N.,  
 RA Cortes J., Leadley P.F.;  
 RT "Analysis of Eryd and ErydII from the erythromycin biosynthetic gene  
 RT cluster in Saccharopolyspora erythraea.";  
 RL Mol. Gen. Genet. 258:78-88 (1998).  
 DR EMBL: Y14327; CAA74702.1; -  
 DR GO: GO:0004553; P:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro: IPR002772; Glyco\_hydro\_3C.  
 DR InterPro: IPR001764; Glyco\_hydro\_3N.  
 DR Pfam: PF00933; Glyco\_hydro\_3; 1.  
 DR Pfam: PF01915; Glyco\_hydro\_3\_C; 1.  
 DR PRINTS: PR00133; GMDPRASE3.  
 SQ SEQUENCE 808 AA; 86677 MW; 0C619016CC00A751 CRC64;

Query Match 64.1%; Score 41; DB 2; Length 808;  
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 DPLTKLWL 10  
 DB 61 DPLAKLWL 68

RESULT 41

07Y308 PRELIMINARY; PRT; 111 AA.  
 ID 07Y308;  
 AC 07Y308;  
 DT 01-OCT-2003 (TREMBLrel. 25, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN RB49ORF095C.  
 OS Enterobacteria phage RB49.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;  
 OC T4-like viruses.  
 CX NCBI\_TaxId=50948;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97250366; PubMed=9096222;  
 RA Monod C., Repolia F., Kutateladze M., Tetaat F., Kirsch H.M.;  
 RT "The genome of the pseudo T-even bacteriophages, a diverse group that

RT resembles T4.";  
 RL J. Mol. Biol. 267:237-249 (1997).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21062343; PubMed=11092834;  
 RA Ang D., Keppel F., Klein G., Richardson A., Georgopoulos C.;  
 RT "Genetic analysis of bacteriophage-encoded coxapronins.";  
 RN Annu. Rev. Genet. 34:439-456 (2000).  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21972795; PubMed=11976309;  
 RA Desplats C., Dez C., Tetaat F., Eleaume H., Kirsch H.M.;  
 RT "Snapshot of the genome of the pseudo-T-even bacteriophage RB49.";  
 RN J. Bacteriol. 184:2789-2804 (2002).  
 RN (4)  
 RP SEQUENCE FROM N.A.  
 RA Tetaat F., Desplats C., Kutateladze M., Monod C., Ackermann H.-W.,  
 RA Kirsch H.M.;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 RN (5)  
 RP SEQUENCE FROM N.A.  
 RA Kirsch H.M.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 RN (6)  
 RP SEQUENCE FROM N.A.  
 RA Ang D., Richardson A., Mayer M.P., Keppel F., Kirsch H.,  
 RA Georgopoulos C.;  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 RN (7)  
 RP SEQUENCE FROM N.A.  
 RA Zhao L., Tetaat F., Kirsch H.M., Arisaka F.;  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 RN (8)  
 RP SEQUENCE FROM N.A.  
 RA Desplats C., Dez C., Tetaat F., Eleaume H., Kirsch H.M.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN (9)  
 RP SEQUENCE FROM N.A.  
 RA Thiemer C.A., Desplats C., Dez C., Tetaat F., Eleaume H., Kirsch H.M.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN (10)  
 RP SEQUENCE FROM N.A.  
 RA Desplats C., Dez C., Tetaat F., Eleaume H., Kirsch H.M.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 RN (11)  
 RP SEQUENCE FROM N.A.  
 RA Kirsch H.M.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 RN (12)  
 RP SEQUENCE FROM N.A.  
 RA Desplats C., Kirsch H.M.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 RN (13)  
 RP SEQUENCE FROM N.A.  
 RA Letarov A.V., Kirsch H.M., Tetaat F.;  
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
 RN (14)  
 RP SEQUENCE FROM N.A.  
 RA Bertrand C., Petrov V., Nolan J., Letarov A., Desplats C., Chin D.,  
 RA Karam J.D., Kirsch H.M.;  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY343333; AA015351.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 111 AA; 13073 MW; 94EB50A5E9E5023D CRC64;

Query Match 62.5%; Score 40; DB 9; Length 111;  
 Best Local Similarity 85.7%; Pred. No. 34;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 DPLTKLWL 9  
 DB 39 DPLTKLWL 45

## RESULT 42

087XC5 PRELIMINARY; PRT; 173 AA.  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE NAD(P)H dehydrogenase, quinone family.  
 GN PEPY04258.  
 OS Pseudomonas syringae (pv. tomato).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=323;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=DC3000;  
 RA Beil R., Ueardar V., Khouri H., Fedorova N., Tran B., Russell D.,  
 RA Berry K., Uteback T., Van Aken S., Feldlym T., Gwin M.,  
 RA Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,  
 RA Brinkac L., Beaman M., Haft D., Selengut J., Nelson W., Davidson T.,  
 RA White O., Fraser C., Collier A.,  
 RT "Complete sequence of Pseudomonas syringae."  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB016871; AA05712.1; -  
 DR TIGR; PEPY04258; -  
 DR GO; GO:0003955; F:NAD(P)H dehydrogenase (quinone) activity; IEA.  
 DR GO; GO:0006118; P:Electron transport; IEA.  
 DR InterPro; IPR003680; NADHdh.2.  
 DR Pfam; PF02525; Flavodoxin\_2; 1.  
 KM Complete proteome.  
 SQ SEQUENCE 173 AA; 19828 MW; F717A393A8607E4B CRC64;

Query Match 62.5%; Score 40; DB 16; Length 173;  
 Best Local Similarity 58.3%; Pred. No. 53;  
 Matches 7; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 WYD--PLTKML 10  
 Db 67 WYNYPLTKML 78

## RESULT 43

0817A3 PRELIMINARY; PRT; 230 AA.

AC 0817A3;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Paired box protein (fragment).  
 GN PAX258.

OS Platyneris dumerilii (Dumeril's clam worm).  
 OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Aciculata;  
 OC Phyllococida; Nereididae; Platyneris.  
 OX NCBI\_TaxID=6359;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RA Zelada F., Burgdorf C., Steimetz P., de Campos-Baptista M.I.M.,  
 RA Witbrodt J., Arend D.;  
 RT "The transition from radial to bilateral symmetry in bilaterian  
 RT ontogeny and evolution."  
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ505023; CAD3608.1; -  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0007275; P:development; IEA.  
 DR InterPro; IPR001523; Paired\_box.  
 DR Pfam; PF00292; PAX; 1.  
 DR PRINTS; PR00027; PAIRDBOX.  
 DR SMART; SM00351; PAX; 1.  
 DR PROSITE; PS00034; PAIRBD\_BOX; 1.  
 FT NON\_TER 1  
 FT NON\_TER 230 1  
 SQ SEQUENCE 230 AA; 24965 MW; D08E417AF3546F17 CRC64;

Query Match 62.5%; Score 40; DB 5; Length 230;  
 Best Local Similarity 75.0%; Pred. No. 71;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYDPLTKL 8  
 Db 210 WFDPLYTKL 217

## RESULT 44

08WST5 PRELIMINARY; PRT; 305 AA.

AC 08WST5;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Gamone 1

GN BLEPHARMONE.  
 OS Blepharisma japonicum.  
 OC Eukaryota; Alveolata; Ciliophora; Heterotricha; Heterotrichida;  
 OC Blepharismidae; Blepharisma.  
 OX NCBI\_TaxID=5961;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=21592973; PubMed=11724922;  
 RA Sugita M., Harumoto T.;  
 RT "Identification, characterization, and complete amino acid sequence of  
 RT the conjugation-inducing glycoprotein (blepharmone) in the ciliate  
 RL Blepharisma japonicum."  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:14446-14451(2001).  
 DR EMBL; AB056596; BAB78725.1; -  
 SQ SEQUENCE 305 AA; 34353 MW; 1DA6C7EA4BFA8B3 CRC64;

Query Match 62.5%; Score 40; DB 5; Length 305;  
 Best Local Similarity 60.0%; Pred. No. 94;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKML 10  
 Db 254 WKDPNNKMWL 263

## RESULT 45

099180 PRELIMINARY; PRT; 345 AA.

AC 099180;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Terminal inverted repeats, and ORF 1.

OS Salmonella typhimurium.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 OX NCBI\_TaxID=602;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=Dublin;  
 RX MEDLINE=91209947; PubMed=1840573;  
 RA Krause M., Harwood J., Flier J., Guiney D.;  
 RT "Genetic analysis of the homology between the virulence plasmids of  
 RT Salmonella dublin and Yersinia pseudotuberculosis."  
 RL Infect. Immun. 59:1860-1863(1991).  
 DR EMBL; M58505; AAA27173.1; -  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0006310; P:DNA recombination; IEA.  
 DR InterPro; IPR001584; Xve.  
 DR Pfam; PF00655; xve; 1.  
 SQ SEQUENCE 345 AA; 40120 MW; EFC1298AD32387C0 CRC64;

Query Match 62.5%; Score 40; DB 2; Length 345;  
 Best Local Similarity 50.0%; Pred. No. 11e+02;  
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```

0Y      1 WYDPLTKLML 10
       | :|: |||
Db      292 WLNPIERLML 301

RESULT 46
ID      053933          PRELIMINARY; PRT; 345 AA.
AC      053933;
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT      01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE      M5 protein (RANSPOSASE of IS630) (Putative integrase protein).
GN      ISO-IS630 OR IS630 OR pSLT042.
OS      Salmonella cholerae-suis (Salmonella enterica),
OS      Salmonella enterica subsp. enterica serovar Choleraesuis, and
OC      Salmonella typhimurium.
CC      Plasmid pKDC50, plasmid 50k virulence, and plasmid pSLT.
CX      Bacteria: Proteobacteria; Gammaproteobacteria; Enterobacteriales;
        Enterobacteriaceae; Salmonella.
        NCBI_Taxid=591, 119912, 602;
        (1)
RP      SEQUENCE FROM N.A.
RC      SPECIES=S.cholerae-suis; STRAIN=RF-1; PLASMID=pKDC50;
RA      Macauli H.;
RL      Submitted (MAR-1992) to the EMBL/genbank/DDBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RC      SPECIES=S.enterica subsp. enterica serovar Choleraesuis; STRAIN=RF-1;
RC      PLASMID=50k virulence;
RA      Okada N., Haneda T.;
RT      "50 kb virulence plasmid of salmonella enterica serovar
RT      Choleraesuis.";
RL      Submitted (MAR-2000) to the EMBL/genbank/DDBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      SPECIES=S.typhimurium; STRAIN=L72 / SGC1412 / ATCC 700720;
RC      PLASMID=pSLT;
RX      MEDLINE=21534948; PubMed=11677609;
RA      McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA      Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D.,
RA      Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvanev E.,
RA      Ryan E., Sun H., Florea L., Miller W., Stonking T., Nhan M.,
RA      Waterston R., Wilson R.K.;
RT      "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT      LT2.";
RL      Nature 413:852-856(2001).
DR      EMBL; D10689; BAAL1531.1; -.
DR      EMBL; AB040415; BAB20556.1; -.
DR      EMBL; AE006471; AAL23461.1; -.
DR      GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR      GO; GO:0003677; F:DNA binding; IEA.
DR      GO; GO:0006310; P:DNA recombination; IEA.
DR      InterPro; IPR001584; Rve.
DR      Pfam; PF00665; rve; 1.
KW      Plasmid; Complete proteome.
SQ      SEQUENCE 345 AA; 40219 MW; E5619391698336D0 CR664;

OY      1 WYDPLTKLML 10
       | :|: |||
Db      292 WLNPIERLML 301

Query Match      62.5%; Score 40; DB 16; Length 345;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

RESULT 47
ID      09M2B5          PRELIMINARY; PRT; 378 AA.
AC      09M2B5;
DT      01-OCT-2000 (TIREMBLrel. 15, Created)

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DT	01-OCT-2003 (Tremblrel. 15, Last sequence update)
DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE	Hypothetical protein.
GN	F23N14_90.
OS	Arabidopsis thaliana (Mouse-ear cress).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsids.
OX	NCBI_TaxID=3702;
RN	(1)
RP	SEQUENCE FROM N.A.
RA	Bloecher H., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X., Quetier F.,
RA	Salanoubat M.;
RL	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN	(2)
RP	SEQUENCE FROM N.A.
RA	EU Arabidopsis sequencing project;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL, AL18638 : CAB83072.1 ; -
DR	PIR, T47407, T47407.
DR	InterPro, IPR001810, F-box.
DR	InterPro, IPR00652, Kelch_rep.
DR	Pfam, PF00646; F-box; 1.
DR	Pfam, PF0344; Kelch; 2.
DR	SMART, SM00256; PBOX; 1.
DR	PROSITE, PS00181; PBOX; 1.
KW	Hypothetical protein.
SO	SEQUENCE 378 AA; 43408 MW; 445B88416A979454 CRC64;
Query Match	
Best Local Similarity	62.5%; Score 40; DB 10; Length 378;
Matches	6; Conservative 0; Mismatches 3; Indels 0; Gaps 0.
Cy	1 WYDPLTKLM 9
Db	280 WYDSEKTLK 288
RESULT 48	
ID	O7TOY2 PRELIMINARY; PRF; 500 AA.
AC	O7TOY2:
DT	01-OCT-2003 (Tremblrel. 25, Created)
DT	01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE	Hypothetical protein.
OS	Xenopus laevis (African clawed frog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Ambiphba; Batrachia; Anura; Mesodactylina; Pipidoidea; Pipidae;
OC	Xenopodinae; Xenopus.
OX	NCBI_TaxID=8355;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Embryo;
EX	Medline=22341132, PubMed=12454917,
RA	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA	Richardson P.;
RT	"Genetic and genomic tools for Xenopus research: The NIH Xenopus
RL	initiative.";
RL	Dev. Dyn. 225:384-391(2002).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Embryo;
EX	Medline=22388257, PubMed=12477932;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA	Achseln S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA	Dickenson L., Marutka K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stadleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Uebin T.B., Toshitaki S., Carninci P., Prange C.C.,
RA	Rana S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy U., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RA Klein S., Strausberg R.,  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC055989; AAK55989.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 500 AA; 54722 MW; 10F16756CAFDC0B CRC64;  
 QY Query Match 62.5%; Score 40; DB 13; Length 500;  
 DB Best Local Similarity 55.6%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 WYDPLTKLM 9  
 DB 248 WYDPLTEW 256  
 RESULT 49  
 Q9VBN4 PRELIMINARY; PRT; 513 AA.  
 ID 09VBN4; Q9VBN4; (TrEMBLrel. 13, Created)  
 DT 01-MAR-2000 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 25, Last annotation update)  
 DE CG15097 protein (GH18278p).  
 GN CG15097.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,  
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.D., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,  
 RA Goadek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Jengam C.,  
 RA Jajaeli M., Kalush F., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Jiamel B.E., Kodira C.D., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,  
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclet J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spindling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svaitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao S., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,  
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
 RA Bazon J., An H., Baldwin D., Bazon J., Beeson K.Y., Busam D.A.,  
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Drenek D., Farfan D.,  
 RA Ferrizera S., Frise E., Galie R.F., Garg N.S., George R.A.,  
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,  
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
 RA Paclet J., Paragas V., Park S., Patel S., Pfeiffer B.,  
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
 RA Stapleton M., Strong R., Svaitskas R., Tector C., Tyler D.,  
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,  
 RT "Sequencing of Drosophila melanogaster genome."  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Prochink S.E., Smith C.D.,  
 RA Clump U.L., Bereman C., Bernan B., Carlson J.W., Celniker S.E.,  
 RA Rump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,  
 RA Searle S.M.J., Smith E., Shu S., Smuchnik F., Whitfield E.,  
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall A., Lewis S.E.,  
 RT "Annotation of Drosophila melanogaster genome."  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.,  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA FlyBase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
 RA Gonzalez M., Guatin H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nunoo J., Paclet J., Paragas V., Park S., Phouanavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.,  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB003798; AAF57630.2; -  
 DR HSSP; 005516; 1CS3  
 DR FLYBASE; FBgn0034396; CG15097.  
 DR GO; GO:0005515; F:protein binding; IEA.  
 DR InterPro; IPR000210; BTB\_POZ.  
 DR InterPro; IPR006651; Kelch.  
 DR InterPro; IPR006652; Kelch\_rep.  
 DR Pfam; PF00651; BTB; 1.  
 DR Pfam; PF01344; Kelch; 6.  
 DR PRINTS; PR00501; KELCHREPAT.  
 DR PROSITE; PSS0097; BTB; 1.  
 SQ SEQUENCE 513 AA; 57551 MW; 20B9D4F732514834 CRC64;  
 QY Query Match 62.5%; Score 40; DB 5; Length 513;  
 DB Best Local Similarity 75.0%; Pred. No. 1.6e+02;



Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 YDPLTKM 9  
 Db 332 YDPLTKM 339

## RESULT 50

09A9X4 PRELIMINARY; PRT; 519 AA.  
 AC 09A9X4;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Hypothetical protein CC0837.  
 GN CC0837.  
 OS Caulobacter crescentus.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;  
 OC Caulobacteraceae; Caulobacter.  
 OX NCBI\_TaxID=155892;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 19089 / CB15;  
 RC MEDLINE=21173698; PubMed=11259647;  
 RA Nieman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,  
 RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohra N., Maddock J.R.,  
 RA Pirochka I., Nelson W.C., Newton A., Stephens C., Madhok N.D., Ely B.,  
 RA Deboy R.T., Dodson R.J., Durkin A.S., Gwin M.L., Haft D.H.,  
 RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,  
 RA Utecherback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,  
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;  
 RT "Complete genome sequence of Caulobacter crescentus."  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).  
 DR EMBL; AE005760; AK22822.1; -.  
 DR TIGR; CC0837; -.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 519 AA; 53934 MW; F37A3A52753DB53B CRC64;

Query Match 62.5%; Score 40; DB 16; Length 519;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 WYDPLTKM 9  
 Db 414 WYAPLAGLM 422

## RESULT 51

08NSC3 PRELIMINARY; PRT; 582 AA.  
 ID 08NSC3;  
 AC 08NSC3;  
 DT 01-OCT-2002 (TREMBLrel. 22, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Similar to intracellular A particle-promoted polypeptide.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=uterus;  
 RA Strauberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR GO; GO:0005515; F:protein binding; ISA.  
 DR InterPro; IPR000210; BTR POZ.  
 DR InterPro; IPR006651; Keich.  
 DR Pfam; PF00651; BTR; 1.  
 DR Pfam; PF01344; Keich; 6.  
 DR PRINTS; PR00501; KEICHPREBAT.

DR SMART; SM00225; BTR; 1.  
 DR SMART; SM00612; Keich; 5.  
 DR PROSITE; PS50097; BTR; 1.  
 SQ SEQUENCE 582 AA; 65620 MW; 0233689DB32E40BD CRC64;

Query Match 62.5%; Score 40; DB 4; Length 582;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YDPLTKM 9  
 Db 363 YDPVTKM 370

## RESULT 52

08SB55 PRELIMINARY; PRT; 612 AA.  
 ID 08SB55;  
 AC 08SB55;  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN OSJNB0091009.4.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Euphorbiaceae; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Euphorbiaceae; Oryzae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wang R.A., Yu Y., Soderlund C., Chen M., Kim H.-R., Rambo T.,  
 RA Sakai C., Henry D., Oates R., Simmons J.;  
 RT "Rice Genomic Sequence."  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC091732; AL77153.1; -.  
 DR Gramene; 08SB55; -.  
 DR InterPro; IPR006928; Glyco\_trans\_6hp.  
 KW Hypothetical protein.  
 SQ SEQUENCE 612 AA; 68316 MW; 077322720C99E444 CRC64;

Query Match 62.5%; Score 40; DB 10; Length 612;  
 Best Local Similarity 58.3%; Pred. No. 1.9e+02;  
 Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 WYD--PLTKML 10  
 Db 419 WYDGMPLRFL 430

## RESULT 53

07XF65 PRELIMINARY; PRT; 612 AA.  
 ID 07XF65;  
 AC 07XF65;  
 DT 01-OCT-2003 (TREMBLrel. 25, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN OSJNB0091009.4.  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Euphorbiaceae; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Euphorbiaceae; Oryzae; Oryza.  
 OX NCBI\_TaxID=39947;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Nipponbare;  
 RA The Rice Chromosome 10 Sequencing Consortium;  
 RT "In-depth view of structure, activity, and evolution of rice  
 chromosome 10."  
 RL Science 300:1566-1569(2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Nipponbare;



DR PROSITE; P550097; BTB; 1.  
 FT NON TER 1  
 SQ SEQUENCE 620 AA; 69069 MW; 47CAD3F3B3A57871 CRC64;

Query Match  
 Best Local Similarity 62.5%; Score 40; DB 5; Length 620;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 YDPLTKLM 9  
 DB 439 YDPLTKLM 446

## RESULT 56

O72V08 PRELIMINARY; PRT; 640 AA.

AC Q72V08; 01-JUN-2003 (TREMBLrel. 24, Created)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Similar to NSI-binding protein.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Osteichthyes; Cypriniformes;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxId=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Body;  
 RA Struhsberg R.;  
 RL Submitted (JAN-2003) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; BC045449; AA045449.1; -;  
 DR GO; GO:0005515; F:protein binding; IEA.  
 DR InterPro; IPR000210; BTB\_POZ.  
 DR InterPro; IPR006651; Kelch.  
 DR InterPro; IPR006652; Kelch\_rep.  
 DR Pfam; PF00651; BTB; 1.  
 DR Pfam; PF01344; Kelch; 6.  
 DR PRINTS; PR00501; KELCHREPEAT.  
 DR SMART; SM00225; BTB; 1.  
 DR SMART; SM00612; Kelch; 6.  
 DR PROSITE; PS50097; BTB; 1.  
 SQ SEQUENCE 640 AA; 71117 MW; DCCGFC2438A1D81 CRC64;

Query Match  
 Best Local Similarity 62.5%; Score 40; DB 13; Length 640;  
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 YDPLTKLM 9  
 DB 482 YDPLTKLM 489

## RESULT 57

O8J2J6 PRELIMINARY; PRT; 648 AA.

AC Q8J2J6; 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Putative aminoacid permease protein.  
 GN AP.

OS Candida albicans (Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
 OX NCBI\_TaxId=5476;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Prignieu O., Porta A., Maresca B.;  
 RL Identification and cloning of the CAP gene of Candida albicans";  
 DR EMBL; AF441396; AAN62330.1; -;  
 DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.  
 DR GO; GO:0006865; P:amino acid transport; IEA.

DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR002293; AA/rel\_permease.  
 DR InterPro; IPR004840; AAC\_permease.  
 DR InterPro; IPR004841; Permease\_region.  
 DR Pfam; PF00324; aa\_permeases; 1.  
 DR PROSITE; PS00218; AMINO ACID PERMEASE 1; 1.

SQ SEQUENCE 648 AA; 71837 MW; A6D2A16EAD5A2B CRC64;

Query Match  
 Best Local Similarity 66.7%; Score 40; DB 3; Length 648;  
 Matches 8; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

OY 1 WY--DPLTKLM 10  
 DB 593 WYLVPLTKFWL 604

## RESULT 58

O8LM21 PRELIMINARY; PRT; 713 AA.

AC O8LM21; 01-OCT-2002 (TREMBLrel. 22, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN OSUNAA0019N10.24.  
 OS Oryza sativa (Japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Eubharoidae; Oryzae; Oryza.  
 OX NCBI\_TaxId=39947;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Nipponbare;  
 RA McCormie W.R., de la Bastide M., Spiegel L., Preston R., Ferraro K.,  
 RA Kuit K., Nascimento L., Zulaevn T., Balija V., Bell M., Baker J.,  
 RA Miller B., Katzenberger F., Muller S., King N., Sullivan P., Yang C.,  
 RA Dile S., O'Shaughnessy A., Palmer L., Dedha N.;  
 RT "Genomic sequence for Oryza sativa, Nipponbare strain, clone  
 OSUNAA0019N10, from chromosome 10, complete sequence."  
 RL Submitted (JUL-2002) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AC124213; AAM74466.1; -;  
 DR Gramene; O8LM21; -;  
 DR InterPro; IPR008928; Glyco\_trans\_6hp.  
 KW Hypothetical protein.

Query Match  
 Best Local Similarity 62.5%; Score 40; DB 10; Length 713;  
 Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

OY 1 WY--DPLTKLM 10  
 DB 520 WYDGMPLRFL 531

## RESULT 59

O8IKY0 PRELIMINARY; PRT; 715 AA.

AC O8IKY0; 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 GN PF14.0471.

OS Plasmodium falciparum (isolate 3D7).  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxId=36329;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=3D7;

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RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Sub B., Peterson J., Angiuoli S.,
RA Partea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.,
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum."
RL Nature 419:498-511(2002).
DR EMBL; AE014824; AAN37084.1; -.
KM Hypothetical protein.
SQ SEQUENCE 715 AA; 84432 MW; 0B80A721D5C3D3B6 CRC64;

Query Match
Best Local Similarity 62.5%; Score 40; DB 5; Length 715;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDP.LTKML 10
DB 53 WYNARTKWL 62

RESULT 60
Q8IK14 PRELIMINARY; PRT; 979 AA.
AC Q8IK14;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DE Hypothetical protein.
PE10 0026
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Sub B., Peterson J., Angiuoli S.,
RA Partea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.,
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum."
RL Nature 419:498-511(2002).
DR EMBL; AE014829; AAN35224.1; -.
KW Hypothetical protein.
SQ SEQUENCE 979 AA; 118671 MW; 273A0810988F5C8F CRC64;

Query Match
Best Local Similarity 62.5%; Score 40; DB 5; Length 979;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDP.LTKML 10
DB 957 WLDALTKQWM 966

RESULT 61
Q87YFO PRELIMINARY; PRT; 283 AA.
AC Q87YFO;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)

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DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Hypothetical protein.
OS PSPPO3850.
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=123;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RA Buell R., Uetendard V., Khouri H., Fedorova N., Tran B., Russell D.,
RA Berry K., Uetendard T., Van Aken S., Feldlym T., Gwin M.,
RA Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
RA Brinkac L., Beaman M., Haft D., Selengut J., Nelson W., Davidsen T.,
RA White O., Fraser C., Collmer A.,
RT "Complete sequence of Pseudomonas syringae."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016869; AA057317.1; -.
DR TIGR; PSPPO3850; -.
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 283 AA; 32710 MW; E6BD39BB099277C4 CRC64;

Query Match
Best Local Similarity 61.7%; Score 39.5; DB 16; Length 283;
Matches 7; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 WYDP.LTKML 10
DB 104 YDPRITRLML 114

RESULT 62
Q91UW3 PRELIMINARY; PRT; 109 AA.
AC Q91UW3;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Isolate hc94 E2 (Genome polypeptide) (fragment).
OS Hepatitis C virus.
OC Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=hc94;
RA Fan X., Di Bisceglie A.M.;
RT "Genetic Characteristics of Putative Hypervariable Region (HVR1) in
RT Genotype 2 Hepatitis C virus."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF218876; AAF80573.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002519; HCV env.
DR InterPro; IPR002531; HCV_NSI.
DR Pfam; PF01539; HCV env; I.
DR Pfam; PF01560; HCV_NSI; I.
DR Prodom; PD186062; HCV_NSI; I.
DR Coab protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polypeptide; Transmembrane.
FT NON TER
SQ SEQUENCE 109 AA; 12115 MW; B04123BF1E056C7A CRC64;

Query Match
Best Local Similarity 60.9%; Score 39; DB 12; Length 109;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDP.LTKML 10
DB 92 YIQPIQLML 101

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RESULT 63
ID 054791 PRELIMINARY; PRT; 155 AA.
AC 054791;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE TSPO protein.
GN TSPO.
OS Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1063;
RN [1]
RP SEQUENCE FROM N.A.
RA Lang H.P.;
RT "Rhodobacter sphaeroides carotenoid genes."
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ010302; CAB38741.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR InterPro: IPR004307; TSPO_MBR.
DR Pfam: PF03073; TSPO_MBR.1.
DR Prodom: PD006774; TSPO_MBR.1.
SQ SEQUENCE 155 AA; 17609 MW; 75A728BBA9CF2C5B CRC64;

Query Match
Best Local Similarity 60.9%; Score 39; DB 2; Length 155;
Best Local Similarity 66.7%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 WYDPLTKLM 9
DB 28 WYDNINKPW 36

RESULT 64
ID 09RC8 PRELIMINARY; PRT; 158 AA.
AC 09RC8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE TSPO.
OS Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1063;
RN [1]
RP SEQUENCE FROM N.A.
RA Choudhary M., Kaplan S.;
RT "DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides 2.4.1."
RL Nucleic Acids Res. 0:0-0(2000).
DR EMBL: AF195123; AAF24291.1; -.
DR PIR: A57438; A57438.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR InterPro: IPR004307; TSPO_MBR.
DR Pfam: PF03073; TSPO_MBR.1.
DR Prodom: PD006774; TSPO_MBR.1.
SQ SEQUENCE 158 AA; 17976 MW; 16569B7156AFD0CD CRC64;

Query Match
Best Local Similarity 60.9%; Score 39; DB 2; Length 158;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 WYDPLTKLM 9
DB 30 WYDNINKPW 38

RESULT 65
O848N8

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ID 0848N8 PRELIMINARY; PRT; 176 AA.
AC 0848N8;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE YabF.
GN YABF.
OS Gamma-Proteobacterium Hoc 75m4.
OC Plasmid pAK116.
OC Bacteria; environmental samples.
OX NCBI_TaxID=77133;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22507661; PubMed=12620823;
RA Knietsch A., Maschke T., Bowen S., Henne A., Daniel R.;
RT "Construction and Screening of Metagenomic Libraries Derived from RT Enrichment Cultures: Generation of a Gene Bank for Genes Confering RT Alcohol Oxidoreductase Activity on Escherichia coli."
RL Appl. Environ. Microbiol. 69:1408-1416(2003).
DR EMBL: AF543470; AA059932.1; -.
DR GO: GO:0046821; C:extrachromosomal DNA; IEA.
DR GO: GO:0003955; F:NAD(P)H dehydrogenase (quinone) activity; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR003680; NADHdh_2.
DR Pfam: PF02525; Flavodoxin_2; 1.
KW Plasmid.
SQ SEQUENCE 176 AA; 20179 MW; ED92C4B3C89FC65 CRC64;

Query Match
Best Local Similarity 60.9%; Score 39; DB 2; Length 176;
Best Local Similarity 58.3%; Pred. No. 80;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

OY 1 WYD--PLTKLM 10
DB 67 WYSTPPLTKLMW 78

RESULT 66
ID 09GLF8 PRELIMINARY; PRT; 177 AA.
AC 09GLF8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Pol protein (Fragment).
GN POL.
OS Trichosurus vulpecula (Brush-tailed possum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
OX NCBI_TaxID=9337;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21105294; PubMed=11160757;
RA Baillie G.J., Wilkins R.J.;
RT "Endogenous Type D Retrovirus in a Marsupial, the Common Brush-tail U. Viroi. 75:2499-2507(2001).
DR EMBL: AF284693; AAG28160.1; -.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0008907; F:integrase activity; IEA.
DR GO: GO:0006310; P:DNA recombination; IEA.
DR InterPro: IPR001037; Integrase_C.
DR Pfam: PF00552; Integrase; 1.
DR Pfam: PF00665; Ite; 1.
FT NON TER
SQ SEQUENCE 177 AA; 20044 MW; A851BD92573E2F6 CRC64;

Query Match
Best Local Similarity 60.9%; Score 39; DB 6; Length 177;
Best Local Similarity 66.7%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 WYDPLTKLM 9
O848N8

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Db 127 WKDPLTHQW 135

## RESULT 67

09CPE6 PRELIMINARY; PRT; 240 AA.

DT 01-JUN-2001 (TRMBLrel. 17, Created)  
DT 01-JUN-2001 (TRMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)

DE HOPD.

GN HOPD OR PM0087.

OS Pasteurella multocida.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

OC Pasteurellaceae; Pasteurella.

OX NCBI\_TaxID=747;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Pm70;

RX MEDLINE=21145866; PubMed=11248100;

RT May B.J., Zhang Q., Li L.L., Paustian M.L., Whitam T.S., Kapur V.,

RL "Complete genomic sequence of Pasteurella multocida Pm70.";

Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

DR EMBL; A5006044; AAK02171.1; -.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.

DR GO; GO:000508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR000045; Peptidase\_A24A.

DR Pfam; PF01478; Peptidase\_A24; 1.

KW Complete proteome.

SQ SEQUENCE 240 AA; 27795 MW; 3FC8C0F8ED8DC9F6 CRC64;

## Query Match

Best Local Similarity 50.0%; Score 39; DB 16; Length 240;

Matches 6; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

Qy 1 WYDPLTKL 10  
Db 229 WYSPMSMKLWI 240

## RESULT 68

096YU1 PRELIMINARY; PRT; 274 AA.

DT 01-DEC-2001 (TRMBLrel. 19, Created)

DT 01-DEC-2001 (TRMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TRMBLrel. 24, Last annotation update)

DE Hypothetical protein ST2085.

GN ST2085.

OS Sulfolobus tokodaii.

OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;

OC Sulfolobus.

OX NCBI\_TaxID=11955;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=JCM 10545 / 7;

RX MEDLINE=21456156; PubMed=11572479;

RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,

RA Sekine M., Baba S.-I., Anai A., Kosugi H., Hosoyama A., Fukui S.,

RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,

RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,

RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,

RA Oshima T., Kikuchi H.,

RT "Complete genome sequence of an aerobic thermophilic

RT Crenarchaeon, Sulfolobus tokodaii strain 7."

RT DNA Res. 8:123-140(2001).

DR EMBL; AP000988; BAB67185.1; -.

DR GO; GO:0016020; C:membrane; IEA.

DR InterPro; IPR000620; DUF6.

DR Pfam; PF00892; DUF6; 2.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 274 AA; 30296 MW; AB4707081FDD2A27 CRC64;

Query Match 60.9%; Score 39; DB 17; Length 274;

Best Local Similarity 75.0%; Pred. No. 1.2e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WYDPLTKL 8  
Db 215 WYDPLTKL 222

## RESULT 69

09LYY7 PRELIMINARY; PRT; 335 AA.

DT 01-OCT-2000 (TRMBLrel. 15, Created)

DT 01-OCT-2000 (TRMBLrel. 15, Last sequence update)

DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)

DE Hypothetical protein.

GN F15A17.10.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eucots II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI\_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Bevan M., Terry N., Ardiles W., Buyschaert C., Dasseville R.,

RA De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,

RA Villarroel R., Gielens J., Van Montagu M., Bancroft I., Mewes H.W.,

RA Rudd S., Lemcke K., Mayer K.F.X.,

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA EU Arabidopsis sequencing project;

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL163002; CAB86065.1; -.

DR PIR; T48319; T48319.

DR InterPro; IPR001810; F-box.

DR InterPro; IPR006652; Kelch\_rep.

DR Pfam; PF00646; F-box; 1.

DR Pfam; PF01344; Kelch; 2.

DR SMART; SM00256; FBOX; 1.

DR SMART; SM00612; Kelch; 1.

DR PROSITE; PS50181; FBOX; 1.

DR Hypothetical protein.

SQ SEQUENCE 335 AA; 38512 MW; CFSBD29DB01DDC26 CRC64;

## Query Match

Best Local Similarity 60.9%; Score 39; DB 10; Length 335;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YDPLTKL 10  
Db 176 YDPLTKL 184

## RESULT 70

09T035 PRELIMINARY; PRT; 365 AA.

DT 01-MAY-2000 (TRMBLrel. 13, Created)

DT 01-MAY-2000 (TRMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)

DE Hypothetical protein.

GN T22F8.190 OR AT4G39290.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eucots II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI\_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Bevan M., Zimmermann W., Gruenisen A., Wambutt R., Bancroft I.,  
 RA Mewes H.W., Mayer K.F.X., Scheller C.,  
 RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Zimmermann W., Gruenisen A., Wambutt R., Kalicki J., Wohlmann P.,  
 RA Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.,  
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AL050351; CAB3644.1; -  
 DR EMBL; AL161595; CAB80592.1; -  
 DR PIR; T08577; T08577.  
 DR InterPro; IPR001810; F-box.  
 DR InterPro; IPR00652; Kelch\_rep.  
 DR Pfam; PF00646; F-box; 1.  
 DR Pfam; PF01344; Kelch; 2.  
 DR SMART; SM00256; FBOX; 1.  
 DR SMART; SM00612; Kelch; 2.  
 KM Hypothetical protein.  
 SQ SEQUENCE 365 AA; 42172 MW; F7187A0F9686E01B CRC64;  
 Query Match 60.9%; Score 39; DB 10; Length 365;  
 Best Local Similarity 55.6%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 WYDPLTKLM 9  
 Db 272 WYDSCRKIM 280  
 RESULT 71  
 Q9W3D5 PRELIMINARY; PRT; 403 AA.  
 AC Q9W3D5;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE CG12081 protein (LD20420P).  
 GN CG12081.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 CC NCB1\_TaxID=7227;  
 CC [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Goeyne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Chame C.R., Pfeiffer B.D.,  
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.M., Miklos G.L.,  
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,  
 RA Ballew R.M., Baer A., Bendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.A., Bouck J., Brockett P., Broctier P.,  
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Dayenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glaeser K.,  
 RA Glöck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwa C.,  
 RA Jalali M., Kalish C.D., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Paclob J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheller F., Shen H.,  
 RA Shie B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svrtkars R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yen R.-F., Zaveli J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster";  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,  
 RA Miranda A., Mungall C.J., Nunoo J., Paclob J., Paragas V., Park S.,  
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celnik S.;  
 RL Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AE003444; AAF46395.1; -  
 DR EMBL; AY119599; AAM50253.1; -  
 DR FLYBase; FBgn0030053; CG12081.  
 DR InterPro; IPR00652; Kelch\_rep.  
 DR Pfam; PF01344; Kelch; 5.  
 SQ SEQUENCE 403 AA; 45202 MW; BEC052258CF3DB95 CRC64;  
 Query Match 60.9%; Score 39; DB 5; Length 403;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Qy 2 YDPLTKLM 9  
 Db 272 FDPRTKLM 279  
 RESULT 72  
 O17702 PRELIMINARY; PRT; 430 AA.  
 AC O17702;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE C53A5.11 protein.  
 GN C53A5.11.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilita; Rhabditoidea;  
 OC Rhabdilitidae; Pelodieridae; Caenorhabditis.  
 CC NCB1\_TaxID=6239;  
 CC [1]  
 RP SEQUENCE FROM N.A.  
 RA Mortimore B.J.;  
 RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=99069613; PubMed=9851916;  
 RX none;  
 RT "Genome sequence of the nematode C.elegans: A platform for  
 RT investigating biology";  
 RT Science 282:2012-2018(1998).  
 DR EMBL; Z81486; CAB03991.1; -  
 DR PIR; T20170; T20170.  
 DR WormPep; C53A5.11; CE08960.

DR GO:0004289; F:subtilase activity; IEA.  
 DR GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro: IPR006652; Kelch\_rep.  
 DR InterPro: IPR00209; Peptidase\_S8.  
 DR Pfam: PF01344; Kelch; 5.  
 DR SMART: SM00612; Kelch; 4.  
 DR PROSITE: PS00136; SUBTILASE ASP; 1.  
 SQ SEQUENCE 430 AA; 48768 MW; 46576AACAD2B8420 CRC64;

Query Match  
 Best Local Similarity 60.9%; Score 39; DB 5; Length 430;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLW 9  
 DB 372 YDPLTKLW 379

RESULT 73  
 ID Q7UA40 PRELIMINARY; PRT; 440 AA.  
 AC Q7UA40;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Putative glycosyltransferase.  
 GN SYN0060.  
 OS Synchococcus sp. (strain WH8102).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synchococcus.  
 OX NCBI\_TaxID=84588;  
 RX MEDLINE=22825697; PubMed=12917641;  
 RA Lamerdin B., Brahamsha B., Larimer F.W., Land M., Hauser L., Chain P.,  
 RA Lamerdin J., Regala W., Allen E.E., McCarron J., Paulsen I.,  
 RT "The genome of a motile marine Synchococcus.";  
 RL Nature 424:1037-1042(2003).  
 DR EMBL: BX569689; CA06575.1; -  
 KW Transference; Complete proteome.  
 SQ SEQUENCE 440 AA; 48530 MW; CA8B56C637E674FA CRC64;

Query Match  
 Best Local Similarity 60.9%; Score 39; DB 16; Length 440;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKM 9  
 DB 31 WYDPMKSLW 39

RESULT 74  
 ID 017700 PRELIMINARY; PRT; 480 AA.  
 AC 017700;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE C53A5.9 protein.  
 GN C53A5.9.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peldertinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Mortimore B.J.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA none;  
 RT "Genome sequence of the nematode C. elegans: A platform for

RT Investigating biology."  
 RL Science 282:2012-2018(1998).  
 DR EMBL: Z81486; CAB03989.1; -  
 DR PIR: T20168; T20168.  
 DR WormPep; C53A5.9; CE08958.  
 DR GO:0005634; C:nucleus; IEA.  
 DR GO:0000074; P:regulation of cell cycle; IEA.  
 DR InterPro: IPR004367; Cyclin\_term.  
 DR InterPro: IPR00651; Kelch.  
 DR InterPro: IPR00652; Kelch\_rep.  
 DR Pfam: PF02984; Cyclin\_C\_1.  
 DR Pfam: PF01344; Kelch; 5.  
 DR PRINTS: PR00501; KELCHREPEAT.  
 DR SMART: SM00612; Kelch; 4.  
 SQ SEQUENCE 480 AA; 5409 MW; 15BD00360B5A199 CRC64;

Query Match  
 Best Local Similarity 60.9%; Score 39; DB 5; Length 480;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLW 9  
 DB 396 YDPLTKLW 403

RESULT 75  
 ID Q88G73 PRELIMINARY; PRT; 518 AA.  
 AC Q88G73;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN PP3852.  
 OS Pseudomonas putida (strain KT2440).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=160488;  
 RX MEDLINE=22423060; PubMed=12534463;  
 RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,  
 RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,  
 RA Brinkac L., Beanan M., Deboy R.T., Daugherty S., Kolonay J.,  
 RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,  
 RA Chris Lee P., Holtzapfle E., Scanlan D., Tran K., Moazzes A.,  
 RA Uteback T., Rizzo M., Lee K., Kosack D., Moestl D., Medler H.,  
 RA Lauber J., Stjepandic D., Hoheisel J., Streitz M., Heim S.,  
 RA Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tnemler B.,  
 RA Frazer C.M.;  
 RT "Complete genome sequence and comparative analysis of the  
 RT metabolically versatile Pseudomonas putida KT2440.";  
 RL Environ. Microbiol. 4:799-808(2002).  
 DR EMBL: AB016788; AAN69446.1; -  
 DR TIGR: PP3852; -

DR GO:0005622; C:intracellular; IEA.  
 DR GO:0005840; C:ribosome; IEA.  
 DR GO:0003735; F:structural constituent of ribosome; IEA.  
 DR GO:0006412; P:protein biosynthesis; IEA.  
 DR InterPro: IPR000595; GMP\_binding.  
 DR InterPro: IPR008195; Ribosomal\_L34E.  
 DR PROSITE: PS00888; GMP\_BINDING\_1; 1.  
 DR PROSITE: PS01145; RIBOSOMAL\_L34E; 1.  
 DR KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 518 AA; 57793 MW; 9314E04F3CC9DB6D CRC64;

Query Match  
 Best Local Similarity 60.9%; Score 39; DB 16; Length 518;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 10  
 DB 244 WYDPMKSLW 253



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RESULT 76
ID 024953 PRELIMINARY; PRT; 551 AA.
AC 024953;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE L-lactate permease (LCTP).
GN HPO141.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kervatage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klein H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Melman J.M., Fujii C., Bowman C., Maithey L., Mallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori."
RL Nature 388:539-547(1997).
DR EMBL; AE000535; AAD07209.1; -.
DR PIR; B64537; B64537.
DR TIGR; HP0141; -.
DR GO; GO:0015129; F:lactate transporter activity; IEA.
DR GO; GO:0015727; P:lactate transport; IEA.
DR InterPro; IPR003804; Lactate perm.
DR Pfam; PF02652; Lactate_perm; 1.
DR TIGRFAMs; TIGR00795; lctp; 1.
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 551 AA; 59407 MW; 3776DA42E7824C7C CRC64;

Query Match 60.9%; Score 39; DB 16; Length 551;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLWL 10
Db 8 YDPLGNLWL 16

RESULT 77
ID 09ZMT9 PRELIMINARY; PRT; 551 AA.
AC 09ZMT9;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE L-lactate permease.
GN LDP 2 OR JHP0129.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Dolg P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
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RT gastric pathogen Helicobacter pylori."
RL Nature 397:176-180(1999).
DR EMBL; AE001452; AAD05719.1; -.
DR PIR; D71969; D71969.
DR GO; GO:0015129; F:lactate transporter activity; IEA.
DR GO; GO:0015727; P:lactate transport; IEA.
DR InterPro; IPR003804; Lactate perm.
DR Pfam; PF02652; Lactate_perm; 1.
DR TIGRFAMs; TIGR00795; lctp; 1.
DR Complete proteome.
SQ SEQUENCE 551 AA; 59533 MW; 1168669180CF9A CRC64;

Query Match 60.9%; Score 39; DB 16; Length 551;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLWL 10
Db 8 YDPLGNLWL 16

RESULT 78
ID 09HFY8 PRELIMINARY; PRT; 837 AA.
AC 09HFY8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Gag protein.
GN Gag.
OS Colletotrichum gloeosporioides (Anthracnose fungus) (Glomerella
OS cingulata).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes; Uncertae sedis; Phyllachorales; Phyllachoraceae;
OC Glomerella.
OX NCBI_TaxID=5457;
RN (1)
RP SEQUENCE FROM N.A.
RC TRANSPOSON=retrotransposon Cgret;
RA Zhu P., Oudemans P.V.;
RT "A long terminal repeat retrotransposon Cgret from the phytopathogenic
RT fungus Colletotrichum gloeosporioides on cranberry."
RL Curr. Genet. 0:0-0(2000)
DR EMBL; AF264028; AAG24791.1; -.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR005162; Retrotrans_gag.
DR InterPro; IPR005159; WCCH.
DR InterPro; IPR001878; ZnF_CCHC.
DR Pfam; PF03732; Retrotrans_gag; 1.
DR Pfam; PF03716; WCCH; 3.
DR Pfam; PF00096; ZF_CCHC; 1.
DR PRINTS; PR00939; C2HCZNFINGER.
DR SMART; SM00343; ZnF_C2HC; 1.
DR PROSITE; PS50158; ZF_CCHC; 1.
SQ SEQUENCE 837 AA; 97738 MW; EF1DABC70FDS5003 CRC64;

Query Match 60.9%; Score 39; DB 3; Length 837;
Best Local Similarity 50.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MYDPLTKLWL 10
Db 161 WEPLQOEML 170

RESULT 79
ID 08A3P6 PRELIMINARY; PRT; 848 AA.
AC 08A3P6;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Conserved hypothetical protein.
```

GN BT2908.  
 OS Bacteroides thetaiotaomicron.  
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
 OC Bacteroidaceae; Bacteroides.  
 OX NCBI\_TaxID=818;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=VPI-5482 / ATCC 29148;  
 RX MEDLINE=2250858; PubMed=12663928;  
 RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,  
 RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."  
 RL Science 299:2074-2076(2003).  
 DR EMBL; AF016938; AAC78014.1; -  
 DR InterPro; IPR006775; DUF608.  
 DR Pfam; PF04685; DUF608; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 848 AA; 96073 MW; DE776292CE6C68F1 CRC64;

Query Match 60.9%; Score 39; DB 16; Length 848;  
 Best Local Similarity 55.6%; Pred. No. 3.8e+02;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 WYDLPTKLM 9  
 DB 255 WFDSLTWVW 263

RESULT 80  
 O9N172 PRELIMINARY; PRT; 871 AA.  
 ID O9N172;  
 AC O9N172;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DR Pol polyprotein (Fragment).  
 GN POL.  
 OS Trichosurus vulpecula (Brush-tailed possum).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.  
 OX NCBI\_TaxID=9337;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21105294; PubMed=11160757;  
 RA Baillie G.J., Wilkins R.J.;  
 RT "Endogenous Type D Retrovirus in a Marsupial, the Common Brush-tail  
 Possum (Trichosurus vulpecula)."  
 RL J. Virol. 75:2499-2507(2001).  
 DR EMBL; AF24725; AAF36395.1; -  
 DR HSSP; P03355; IMML.  
 DR GO; GO:0004182; F:carboxypeptidase A activity; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0008907; F:integrase activity; IEA.  
 DR GO; GO:0004523; F:ribonuclease H activity; IEA.  
 DR GO; GO:0003723; F:RNA binding; IEA.  
 DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0008270; F:zinc ion binding; IEA.  
 DR GO; GO:0015074; F:DNA recombination; IEA.  
 DR GO; GO:0006310; F:DNA replication; IEA.  
 DR GO; GO:0006278; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR001037; Integrase\_C.  
 DR InterPro; IPR000834; Peptidase\_M14.  
 DR InterPro; IPR002156; Peptidase\_M14.  
 DR InterPro; IPR001584; RVE.  
 DR InterPro; IPR000477; RVTse.  
 DR Pfam; PF00552; Integrase; 1.  
 DR Pfam; PF02022; Integrase\_Zn; 1.  
 DR Pfam; PF00075; rnaaseH; 1.  
 DR Pfam; PF00665; rve; 1.  
 DR Pfam; PF00078; rvc; 1.

DR PROSITE; PS00133; CARBOXYPEPT\_ZN\_2; 1.  
 KW Polypeptide; RNA-directed DNA polymerase; Transferase.  
 FT NON\_TER  
 SQ SEQUENCE 871 AA; 98235 MW; 839AE439025C1543 CRC64;

Query Match 60.9%; Score 39; DB 6; Length 871;  
 Best Local Similarity 66.7%; Pred. No. 3.9e+02;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 WYDLPTKLM 9  
 DB 821 WKDPLTHQW 829

RESULT 81  
 O9TTA5 PRELIMINARY; PRT; 941 AA.  
 ID O9TTA5;  
 AC O9TTA5;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DR DNA-dependent ATPase A.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Thymus;  
 RX MEDLINE=20179861; PubMed=10713074;  
 RA Muthuswami R., Truman P.A., Mesner L.D., Hockensmith J.W.;  
 RT "A Eukaryotic SM12/SNP2 Domain, an Exquisite Detector of Double-  
 stranded to Single-stranded DNA Transition Elements."  
 RL J. Biol. Chem. 275:7648-7655(2000).  
 DR EMBL; AF173643; AAF22285.1; -  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0008026; F:ATP dependent helicase activity; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0016787; F:hydrolyase activity; IEA.  
 DR InterPro; IPR001410; DEAD.  
 DR InterPro; IPR001650; Helicase\_C.  
 DR InterPro; IPR000330; SNF2\_N.  
 DR Pfam; PF00271; Helicase\_C; 1.  
 DR Pfam; PF00176; SNF2\_N; 2.  
 DR SMART; SM00487; DEXDC; 1.  
 DR SMART; SM00490; HELIC; 1.  
 KW ATP-binding; Helicase; Hydrolase.  
 SQ SEQUENCE 941 AA; 104915 MW; AC309EF813B931B CRC64;

Query Match 60.9%; Score 39; DB 6; Length 941;  
 Best Local Similarity 75.0%; Pred. No. 4.2e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 YDPLTKLM 9  
 DB 267 YDPLTKLM 274

RESULT 82  
 O8XX42 PRELIMINARY; PRT; 948 AA.  
 ID O8XX42;  
 AC O8XX42;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DR Putative signal peptide protein.  
 GN RSC2276 OR RS01282.  
 OS Ralstonia solanacearum (Pseudomonas solanacearum).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Burkholderiaceae; Ralstonia.  
 OX NCBI\_TaxID=305;  
 RN (1)

RP SEQUENCE FROM N.A.  
 RC STRAIN=GM1100;  
 RX MEDLINE=21681879; PubMed=11823852;  
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,  
 Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,  
 Chandelier M., Choise N., Claudel-Renard C., Cunac S., Demange N.,  
 Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,  
 Signier P., Thebaud P., Whalen M., Wincker P., Levy M.,  
 RA Weissbach J., Boucher C.A.;  
 RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*";  
 RL Nature 415:497-502(2002).  
 DR EMBL; AL646069; CAD15983.1; -  
 KW Complete proteome.  
 SQ SEQUENCE 948 AA; 103933 MW; D3ED825F08A8E48 CRC64;

QY Query Match 60.9%; Score 39; DB 16; Length 948;  
 Best Local Similarity 60.0%; Pred. No. 4.3e+02;  
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1 WYDPLTKML 10  
 101 WYQALPKAML 110

RESULT 83  
 ID 086585 PRELIMINARY; PRT; 2183 AA.  
 AC 086585;  
 DT 01-NOV-1998 (TRENBLrel. 08, Created)  
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Hypothetical protein SCO6220.  
 GN SCO6220 OR SC2H4.02.  
 OS Streptomyces coelicolor.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycinae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2) / M145;  
 RX MEDLINE=21996410; PubMed=12000953;  
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,  
 Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,  
 Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
 Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
 Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,  
 Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,  
 Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,  
 RA Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomycete *Streptomyces*  
 coelicolor A3(2).";  
 RL Nature 417:141-147(2002).  
 DR EMBL; AL939126; CA20596.1; -  
 DR PIR; T37218; T37218.  
 DR InterPro; IPR006530; YD.  
 DR Pfam; PF05593; RNS\_repeat; 6.  
 DR TIGRFAMs; TIGR01643; YD\_repeat\_2x; 9.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 2183 AA; 233388 MW; 373B8EA2BC998FD CRC64;

QY Query Match 60.9%; Score 39; DB 16; Length 2183;  
 Best Local Similarity 66.7%; Pred. No. 9.7e+02;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 1 WYDPLTKML 9  
 1942 WYQALPKML 1950

RESULT 84  
 ID 07UT29 PRELIMINARY; PRT; 277 AA.

AC 07UT29;  
 DT 01-OCT-2003 (TRENBLrel. 25, Created)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN RB4150.  
 OS Rhodospirillum rubrum.  
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;  
 OC Planctomycetaceae; Firellula.  
 OX NCBI\_TaxID=117;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1;  
 RX MEDLINE=22735913; PubMed=12835416;  
 RA Glockner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,  
 RA Ludwig W., Gade D., Beck A., Borzym K., Hellmann K., Rabus R.,  
 RA Schlesner H., Amann R., Reinhardt R.;  
 RT "Complete genome sequence of the marine planctomycete *Firellula* sp.  
 strain 1";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).  
 DR EMBL; BX294140; CAD73612.1; -  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 277 AA; 31373 MW; FABD51A3D984B11C CRC64;

QY Query Match 60.2%; Score 38.5; DB 16; Length 277;  
 Best Local Similarity 53.8%; Pred. No. 1.5e+02;  
 Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

Db 1 WYD--P-LTKML 10  
 64 WYDMMBPQKIKML 76

RESULT 85  
 ID P71125 PRELIMINARY; PRT; 33 AA.  
 AC P71125;  
 DT 01-FEB-1997 (TRENBLrel. 02, Created)  
 DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 DE lcp protein (Fragment).  
 GN lcp.  
 OS Campylobacter jejuni.  
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;  
 OC Campylobacteraceae; Campylobacter.  
 OX NCBI\_TaxID=197;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=81-176;  
 RX MEDLINE=96239019; PubMed=8675309;  
 RA Pickett C.L., Pesci E.C., Cottle D.L., Russell G., Erdem A.N.,  
 RA Zeytin H.;  
 RT "Prevalence of cytolethal distending toxin production in *Campylobacter*  
 jejuni and relatedness of *Campylobacter* sp. cdtB gene.";  
 RL Infect. Immun. 64:2070-2078(1996).  
 DR EMBL; U51121; AAB06710.1; -  
 FT NON\_TER 33  
 SQ SEQUENCE 33 AA; 3859 MW; C6A46123212DAF4D CRC64;

QY Query Match 59.4%; Score 38; DB 2; Length 33;  
 Best Local Similarity 55.6%; Pred. No. 23;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 2 YDPLTKML 10  
 8 YDPSNIML 16

RESULT 86  
 ID 08F6Y0 PRELIMINARY; PRT; 43 AA.  
 AC 08F6Y0;  
 DT 01-MAR-2003 (TRENBLrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Hypothetical protein.  
GN L1169.  
OS Leptospira interrogans.  
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.  
OX NCBI\_TaxID=173;  
[1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;  
RA Ren S.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AE011300; AAA8368.1; -;  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 43 AA; 5302 MW; 49473435BFAD790C CRC64;  
  
Query Match 59.4%; Score 38; DB 16; Length 43;  
Best Local Similarity 55.6%; Pred. No. 29;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
OY 1 WYDPLTKLML 9  
Db 14 FYEPTLKLM 22  
  
RESULT 87  
ID Q8W3Q4 PRELIMINARY; PRT; 92 AA.  
AC Q8W3Q4;  
DT 01-MAR-2002 (TREMBlrel. 20, Created)  
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE Reverse transcriptase (Fragment).  
GN NOR3.  
OS Silene noctiflora (night-flowering catchfly).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllales; Caryophyllaceae; Silene.  
OX NCBI\_TaxID=39899;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TRANSPOSON=Ty1-copia type retrotransposon;  
RA Matsunaga S.;  
RL "Retrotransposons in the genus Silene."  
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB065075; BAB83582.1; -;  
FT NON TER 1 1  
SQ SEQUENCE 92 AA; 10696 MW; 1040F21BBA53DDB9 CRC64;  
  
Query Match 59.4%; Score 38; DB 10; Length 92;  
Best Local Similarity 70.0%; Pred. No. 63;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
OY 1 WYDPLTKLML 10  
Db 51 WYDRLSKLL 60  
  
RESULT 88  
ID Q8EUP0 PRELIMINARY; PRT; 140 AA.  
AC Q8EUP0;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Hypothetical protein.  
GN MYB8810.  
OS Mycoplasma penetrans.  
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
OX NCBI\_TaxID=28227;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=HF-2;  
RX MEDLINE=22354719; PubMed=12466555;  
RA Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,  
RA Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.,  
RT "The complete genomic sequence of Mycoplasma penetrans, an  
RT intracellular bacterial pathogen in humans."  
RL Nucleic Acids Res. 30:5293-5300(2002).  
DR EMBL: AP004173; BAC44672.1; -;  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 140 AA; 16102 MW; 67EA45710F80FPA1 CRC64;  
  
Query Match 59.4%; Score 38; DB 16; Length 140;  
Best Local Similarity 55.6%; Pred. No. 95;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
OY 2 WYDPLTKLML 10  
Db 39 YNPITKQWI 47  
  
RESULT 89  
ID Q9K9C7 PRELIMINARY; PRT; 190 AA.  
AC Q9K9C7;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Hypothetical protein BH2722.  
GN BH2722.  
OS Bacillus halodurans.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=86665;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C-125 / JCM 9153;  
RX MEDLINE=20512582; PubMed=11058132;  
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,  
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kohara S.,  
RA Horikoshi K.,  
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus  
RT halodurans and genomic sequence comparison with Bacillus subtilis."  
RL Nucleic Acids Res. 28:4317-4331(2000).  
DR EMBL: AP001516; BAB06441.1; -;  
DR PIR: B83990; B83990.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 190 AA; 21477 MW; 626CE4855E2C3A4F CRC64;  
  
Query Match 59.4%; Score 38; DB 16; Length 190;  
Best Local Similarity 70.0%; Pred. No. 1.3e+02;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
OY 1 WYDPLTKLML 10  
Db 146 WTVDTLTKLML 155  
  
RESULT 90  
ID Q27482 PRELIMINARY; PRT; 206 AA.  
AC Q27482;  
DT 01-JAN-1998 (TREMBlrel. 05, Created)  
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Hypothetical protein MTH1433.  
GN MTH1433.  
OS Methanobacterium thermoautotrophicum.  
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;  
OC Methanobacteriaceae; Methanothermobacter.  
OX NCBI\_TaxID=187420;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Delta H;  
RX MEDLINE=98037514; PubMed=9371463;

RA Smith D.R., Doucette-Stamm L.A., Delonguey C., Lee H.-M., Dubois J.,  
RA Altriede T., Bahirzadeh R., Blakely D., Cook R., Gilbert K.,  
RA Harrison D., Hoang L., Keagle P., Lunn W., Pochter J., Qiu D.,  
RA Spadafora R., Viicare R., Wang Y., Wierdowski J., Gibson R.,  
RA Jiwani N., Carnue A., Bush D., Safer H., Patwell D., Prabhakar S.,  
RA Mcougall S., Shmer G., Goyal A., Petrovski S., Church G.M.,  
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;  
RT "Complete genome sequence of Methanobacterium thermoautotrophicum  
RT deltaH: functional analysis and comparative genomics.";  
RL J. Bacteriol. 179:7135-7155 (1997).  
DR EMBL; AE000905; AAB85908.1; -.  
DR PIR; G69057; G69057.  
KM Hypothetical protein; Complete proteome.  
SQ SEQUENCE 206 AA; 21815 MW; 5982982950518AEE CRC64;

Query Match 59.4%; Score 38; DB 17; Length 206;  
Best Local Similarity 75.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YDPLTKLM 9  
Db 106 YDPLTKLM 113

RESULT 91  
ID 08A620 PRELIMINARY; PRT; 283 AA.  
AC 08A620;  
DT 01-JUN-2003 (TRENBLrel. 24, Created)  
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE Putative oxidoreductase.  
GN BT2066.  
OS Bacteroides thetaiotaomicron.  
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
OC Bacteroidaceae; Bacteroides.  
OX NCBI\_TaxID=818;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VPI-5482 / ATCC 29148;  
RX MEDLINE=22550858; PubMed=12663928;  
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,  
RA Chiang H.C., Hooper L.V., Gordon J.I.;  
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";  
RL Science 299:2074-2076 (2003).  
DR EMBL; AE016934; AA077173.1; -.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro: IPR002198; ADH\_short.  
DR Pfam; PF00106; adh\_short; 1.  
KM Complete proteome.  
SQ SEQUENCE 283 AA; 31619 MW; BDE4DFB5A3C544 CRC64;

Query Match 59.4%; Score 38; DB 16; Length 283;  
Best Local Similarity 55.6%; Pred. No. 1.9e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9  
Db 209 WYDPLTKLM 217

RESULT 92  
ID 016974 PRELIMINARY; PRT; 295 AA.  
AC 016974;  
DT 01-JAN-1998 (TRENBLrel. 05, Created)  
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
GN T02B11.1.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;

OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RA None;  
RT "Genome sequence of the nematode C. elegans: a platform for  
RT investigating biology. The C. elegans Sequencing Consortium.";  
RL Science 282:2012-2018 (1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Goela D.;  
RT "The sequence of C. elegans cosmid T02B11.";  
RT Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Waterston R.;  
RT "Direct Submission.";  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF022979; AAB69903.1; -.  
DR PIR; T32202; T32202.  
DR WormPep; T02B11.1; CE13032.  
KM Hypothetical protein.  
SQ SEQUENCE 295 AA; 34613 MW; 24613CA68AFB8543 CRC64;

Query Match 59.4%; Score 38; DB 5; Length 295;  
Best Local Similarity 85.7%; Pred. No. 2e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 PLTKLMT 10  
Db 3 PLTKLMT 9

RESULT 93  
ID 09N3X5 PRELIMINARY; PRT; 300 AA.  
AC 09N3X5;  
DT 01-OCT-2000 (TRENBLrel. 15, Created)  
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE Serpentine receptor, class 9 (Gamma) protein 50.  
GN Y43B11AR.2 OR SRG-50.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RA Wilson R.;  
RT "Genome sequence of the nematode C. elegans: a platform for  
RT investigating biology. The C. elegans Sequencing Consortium.";  
RL Science 282:2012-2018 (1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Cordes M., Maupin R.;  
RT "The sequence of C. elegans cosmid Y43B11AR.";  
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Waterston R.H.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Waterston R.;



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SQ SEQUENCE 341 AA; 38032 MW; 0AF98BB343B75774 CRC64;
Query Match 59.4%; Score 38; DB 16; Length 341;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DPLTKLW 9
    |||:|
    184 DPLTKLW 190

RESULT 97
08BJT8 PRELIMINARY; PRT; 345 AA.
ID 08BJT8
AC 08BJT8
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE GAF domain/GGDEF domain protein.
GN PP2505.
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weiner C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
RA Madupu R., Nelson W., White O., Peterson J., Khouli H., Hance I.,
RA Chris Lee P., Holtzapfel E., Scanlan D., Tran K., Moazzez A.,
RA Uterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
RA Lauder J., Stjepandic D., Hohnselt U., Straetz M., Heim S.,
RA Kiewitz C., Eissen J., Timmis K.N., Diesterhoef A., Thiemler B.,
RA Fraser C.M.;
RA "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808(2002).
DR EMBL; AE016783; AAN68117.1; -.
DR TIGR; PP2505; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0008170; F:N-methyltransferase activity; IEA.
DR GO; GO:0006306; P:DNA methylation; IEA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR00160; GGDEF.
DR Pfam; PF00590; GAF.1.
DR Pfam; PF00990; GGDEF.1.
DR PROSITE; PS00887; GGDEF.1.
DR PROSITE; PS00092; N6_MTHASE.1.
DR Complete proteome.
SQ SEQUENCE 345 AA; 38521 MW; 89EC3F871D000D0C CRC64;

Query Match 59.4%; Score 38; DB 16; Length 345;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DPLTKLW 9
    |||:|
    184 DPLTKLW 190

RESULT 98
08JDY9 PRELIMINARY; PRT; 361 AA.
ID 08JDY9
AC 08JDY9
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE ATase VIRB11 homolog.
GN BMEI10035.
OS Brucella melitensis.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688;
RA Delvecchio V.G., Kapratel V., Redkar R.J., Patra G., Muijer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonksi L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-D.,
RA Haselkorn R., Kyriides N., Overbeek R.;
RA "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL; AE009642; AAL53276.1; -.
DR PIR; A13513; A13513.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR GO; GO:000437; GSP11 E.1.
DR InterPro; IPR001482; GSP11 E.
DR Pfam; PF00437; GSP11 E.1.
DR PROSITE; PS00675; SIGMA54_INTERACT_1; 1.
DR Complete proteome.
SQ SEQUENCE 361 AA; 40723 MW; 43D97E87A99E3B7D CRC64;

Query Match 59.4%; Score 38; DB 16; Length 361;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WYDPLTK 7
    |||:|
    343 WYDPLTK 349

RESULT 99
08FXK7 PRELIMINARY; PRT; 361 AA.
ID 08FXK7
AC 08FXK7
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Type IV secretion system protein VirB11.
GN BRA0059.
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=1330 / Biovar 1;
RX MEDLINE=22247741; PubMed=12271122;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eissen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Unayam L., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Krahl M., Shetty J., Malek J., Van Aken S.B.,
RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
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RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
DR EMBL; AE014510; AAN33271.1; -.
DR TIGR; BRA0059; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR GO; GO:000437; GSP11 E.
DR InterPro; IPR001482; GSP11 E.

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DR InterPro: IPR002078; Sig54\_interact.  
 DR Pfam: PF00437; GSP1\_E; 1.  
 DR ProDom: PD000739; GSP1\_E; 1.  
 DR PROSITE: PS00675; SIGMA54\_INTERACT\_1; 1.  
 KW Complete proteome.  
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 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
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 RP SEQUENCE FROM N.A.  
 RC STRAIN=2308;  
 RX MEDLINE=20398168; PubMed=10940027;  
 RA Sieira R., Comercl D.J., Sanchez D.O., Ugalde R.A.;  
 RT "A Homologue of an Operon Required for DNA Transfer in Agrobacterium  
 RT is Required in Brucella abortus for Virulence and Intracellular  
 RT Multiplication.";  
 RL J. Bacteriol. 182:4849-4855(2000).  
 DR EMBL: AF226278; AAF73904.1; -.  
 DR GO: GO:0005622; C:intracellular; IEA.  
 DR GO: GO:0005524; P:ATP binding; IEA.  
 DR GO: GO:0003677; F:DNA binding; IEA.  
 DR GO: GO:0006810; P:transport; IEA.  
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 DR ProDom: PD000739; GSP1\_E; 1.  
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